

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:30:49 ; Search time 408 Seconds

(without alignments)
8971.662 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggtttcaagatacagct.....atgcgcagtaoagttggttag 1356

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 19Jun03.*
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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1356	100.0	1356	21	Sequence encoding
2	1340	98.8	1605	21	F. graminearum tri
3	915.6	67.5	1403	21	Sequence encoding
4	915.6	67.5	12949	21	Transformation vec
5	915.6	67.5	13737	21	Transformation vec
6	249.8	18.4	1425	21	Sequence encoding
7	146.2	10.8	695	21	Aspergillus oryzae
8	116.2	8.6	482	25	Aspergillus oryzae

9	39.8	2.9	4403765	22	AA199683	Mycobacterium tube
10	39.8	2.9	4411529	22	AA199682	Mycobacterium tube
11	36.4	2.7	1605	17	AAT37310	Aromatic acyl tran
c 12	35.6	2.6	1459	24	ABQ33692	Oligonucleotide fo
13	35.6	2.6	1459	24	ABQ33693	Oligonucleotide fo
c 14	35.6	2.6	1463	24	ABQ14442	Oligonucleotide fo
15	35.6	2.6	1463	24	ABQ14443	Oligonucleotide fo
16	35.4	2.6	34980	22	AAH41223	Pyrococcus abyssi
17	34.2	2.5	7234	23	AA574818	DNA encoding novel
18	34	2.5	369	25	ABZ40050	N. gonorrhoeae nuc
c 19	34	2.5	3115	24	ABQ43652	Oligonucleotide fo
c 20	34	2.5	3115	24	ABQ43653	Oligonucleotide fo
21	34	2.5	26223	22	AAF28554	Genomic fragment #
c 22	33.8	2.5	1077	23	AA593503	DNA encoding novel
23	33.8	2.5	2899	22	AAH02926	Human shear stress
24	33.8	2.5	2955	24	ABN95650	Gene #2148 used to
25	33.8	2.5	2955	25	ABZ75899	Heart disease targ
26	33.8	2.5	3075	24	AA594880	Human DNA sequence
c 27	33.8	2.5	21567	23	AA59514	Propionibacterium
28	33.6	2.5	1737	23	ABL56857	Rice derived plant
29	33.6	2.5	1737	24	ABQ82682	Rice blight resist
30	33.4	2.5	675	22	AAH68266	C glutamicum codin
31	33.4	2.5	675	25	ACA01814	C. glutamicum deri
32	33.4	2.5	2997	18	AAT93597	Emeria tenella sp
33	33.4	2.5	3094	10	AA592579	Sequence of the 1.
34	33.4	2.5	3094	18	AAT93596	Emeria tenella sp
c 35	33.4	2.5	4098	23	ABL41555	Fusion gene of tre
c 36	33.4	2.5	4716	23	ABL41560	Fusion gene of tre
c 37	33.4	2.5	6977	14	AAQ35900	Polyhydroxyalkanoa
c 38	33.4	2.5	305400	22	AAH68534	C glutamicum codin
c 39	33.4	2.5	34980	24	ABQ81845	Bifidobacterium lo
c 40	33.2	2.4	701	24	ABQ17898	Oligonucleotide fo
41	33.2	2.4	701	24	ABQ17899	Oligonucleotide fo
c 42	33.2	2.4	938	24	ABQ42724	Oligonucleotide fo
c 43	33.2	2.4	938	24	ABQ42725	Oligonucleotide fo
c 44	33.2	2.4	939	24	ABQ42118	Oligonucleotide fo
45	33.2	2.4	939	24	ABQ42119	Oligonucleotide fo

ALIGNMENTS

RESULT 1	AA54209	ID	AAA54209	standard; DNA; 1356 BP.
XX	AA54209;	AC	AA54209;	
XX		XX		
DT	26-FEB-2001	(first entry)		
XX		XX		
DE	Sequence encoding trichothecene resistance polypeptide.			
XX		XX		
KW	Trichothecene resistance; resistant; crop protection; mycotoxin;			
KW	fungus; wheat; maize; barley; rice; heterologous gene;			
KW	transformation; Fusarium; ds.			
XX		XX		
OS	Fusarium graminearum.			
XX		XX		
PH	Key	Location/Qualifiers		
FT	CDS	1..1356		
FT		/*tag= a		
FT		/product= Trichothecene resistance polypeptide		
XX		XX		
PN	WC200060061-A2.			
XX		XX		
PD	12-OCT-2000.			
XX		XX		
PF	29-MAR-2000; 2000WO-EP02769.			
XX		XX		
PR	31-MAR-1999; 99US-0282995.			
PR	11-FEB-2000; 2000US-0502852.			
XX		XX		
PA	(NOVS) NOVARTIS AG.			

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX P-PSDB; AAB03935.
DR WPI; 2000-679374/66.
XX Plant cell for preventing mycotoxin contamination of wheat, maize,
PT barley or rice plant, comprises heterologous polynucleotide encoding
PT gene product expressed in cell, having trichothecene resistance
PT activity
XX
XX Claim 8; Page 48-49; 62pp; English.
XX A heterologous gene encoding a gene product which confers
CC trichothecene resistance can be used to transform plant cells to
CC make them resistant to fungal infection. The transformation method is
CC useful for preventing mycotoxin contamination of a plant,
CC particularly a crop plant such as wheat, maize, barley or rice, and
CC for reducing and/or preventing the growth of a fungus of the genus
CC Fusarium that produces a trichothecene, preferably comprising a C-3
CC hydroxyl group, by growing transformed crop plants in an area which
CC is moderate to severe fungal infestation.
XX
SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 other;
Query Match 100.0%; Score 1356; DB 21; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTTCAAGATACAGCTCGACACCTCGGCCAGCTACGAGCCTCCTTTTCGATCTAC 60
DB 1 ATGGCTTCAAGATACAGCTCGACACCTCGGCCAGCTACGAGCCTCCTTTTCGATCTAC 60
QY 61 ACCCAATCAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCACTATTGTGACG 120
DB 61 ACCCAATCAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCACTATTGTGACG 120
QY 121 ACCTTGAGCAAGGCTTAAAGCGTCTTCGAAAGCGTCCGATGGGTGCGAGGCCAGTTC 180
DB 121 ACCTTGAGCAAGGCTTAAAGCGTCTTCGAAAGCGTCCGATGGGTGCGAGGCCAGTTC 180
QY 181 AAGCCGAGGCGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGGAGAC 240
DB 181 AAGCCGAGGCGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGGAGAC 240
QY 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
DB 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
QY 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGAAGAGAACATATCGCGCCAGGAAG 360
DB 301 ATGAGAAAGCGGGATACCTATGGCGATGTTTGAAGAGAACATATCGCGCCAGGAAG 360
QY 361 ACGTTACTATTGACCTGTGACTGCTGCTCCGACGACCCAAAGCTGTAATTCATTTCGAG 420
DB 361 ACGTTACTATTGACCTGTGACTGCTGCTCCGACGACCCAAAGCTGTAATTCATTTCGAG 420
QY 421 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGACAGCAGCGTGTATGGAT 480
DB 421 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGACAGCAGCGTGTATGGAT 480
QY 481 ATGTTAGCCCAAGATGCGGTGATCCGCTACTCTCCAAAGCGTCCGTAAGCCCAATTC 540
DB 481 ATGTTAGCCCAAGATGCGGTGATCCGCTACTCTCCAAAGCGTCCGTAAGCCCAATTC 540
QY 541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGAGATAGTTCCTTACTCTTCAA 600
DB 541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGAGATAGTTCCTTACTCTTCAA 600
QY 601 AACTATACGATTGCCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGTGGT 660
DB 601 AACTATACGATTGCCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGTGGT 660

QY 661 GACGCTGTTCTCAGCCCGGTGAGTGAAGCTGGCGTCTTCTCAATTCAGCCCAAGGCC 720
DB 661 GACGCTGTTCTCAGCCCGGTGAGTGAAGCTGGCGTCTTCTCAATTCAGCCCAAGGCC 720
QY 721 ATGTGAGAGCTCAAGAGTCTGCTACCAAGACTCTTGAAGCATCAACAAGTTCGTGTCG 780
DB 721 ATGTGAGAGCTCAAGAGTCTGCTACCAAGACTCTTGAAGCATCAACAAGTTCGTGTCG 780
QY 781 ACTGAGAGTCTTTCGGCGTTCATCTGGAATCGGCTCTCGCGTGGTCTCGAAAGA 840
DB 781 ACTGAGAGTCTTTCGGCGTTCATCTGGAATCGGCTCTCGCGTGGTCTCGAAAGA 840
QY 841 ATCGATGGCTCTGCACTACCGAGTTCCTGCGTGTCTGATGCTCGACCGCAATGGGT 900
DB 841 ATCGATGGCTCTGCACTACCGAGTTCCTGCGTGTCTGATGCTCGACCGCAATGGGT 900
QY 901 GTCTCGAAACAATACCCAGGCTTCTTAAACATCACTCAACAATCGACATCGACATCGC 960
DB 901 GTCTCGAAACAATACCCAGGCTTCTTCAAAAATGACCTTACCACAACTCGACATCGC 960
QY 961 GAAATCGCCAAAGAGTCACTCGGCGCAACAGCATCAAGCTTCGTTGAGAACTCGACCCC 1020
DB 961 GAAATCGCCAAAGAGTCACTCGGCGCAACAGCATCAAGCTTCGTTGAGAACTCGACCCC 1020
QY 1021 GCGAGCATGCGCCAGCGAAACAGAGGTCTCGGACGTCTGCAACAACACCCGCAAG 1080
DB 1021 GCGAGCATGCGCCAGCGAAACAGAGGTCTCGGACGTCTGCAACAACACCCGCAAG 1080
QY 1081 TCCAAAGTATTCCTGAGCGGTGATGCGGACCCATCTACGAGCGTCACTGAGTCTTGG 1140
DB 1081 TCCAAAGTATTCCTGAGCGGTGATGCGGACCCATCTACGAGCGTCACTGAGTCTTGG 1140
QY 1141 GCCAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGAGTGAAGCCCGAGACTGTG 1200
DB 1141 GCCAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGAGTGAAGCCCGAGACTGTG 1200
QY 1201 AGACGCGCAATCTTTCAGCGCTTGTGAGAGCTTGTATGTATGCTTATGCCCAAGAGCCTGAT 1260
DB 1201 AGACGCGCAATCTTTCAGCGCTTGTGAGAGCTTGTATGTATGCTTATGCCCAAGAGCCTGAT 1260
QY 1261 GCGAGTTCCTGCGCGCTTCTCTGAGGAGTGAAGATGAGACCGATGAGAGCGGAT 1320
DB 1261 GCGAGTTCCTGCGCGCTTCTCTGAGGAGTGAAGATGAGACCGATGAGAGCGGAT 1320
QY 1321 AAGGATGAGCAAGTATGCGAGTACGTTGGTTAG 1356
DB 1321 AAGGATGAGCAAGTATGCGAGTACGTTGGTTAG 1356
RESULT 2
AAZ89368 standard; DNA; 1605 BP.
ID AAZ89368
XX
AC AAZ89368;
XX
DT 09-JUN-2000 (first entry)
XX
DE F. graminearum trichothecene 3-O-acetyltransferase DNA.
XX
KW Trichothecene 3-O-acetyltransferase; selective marker; ds.
XX
OS Fusarium graminearum.
XX
FH Location/Qualifiers
FT CDS 135..1490
FT /*tag= a
FT /product= "trichothecine 3-O-acetyltransferase"
XX
PN JP2000032985-A.
XX
PD 02-FEB-2000.
XX

12-OCT-2000.
 29-MAR-2000; 2000WO-EP02769.
 31-MAR-1999; 99US-0282995.
 11-FEB-2000; 2000US-0502852.
 (NOVS) NOVARTIS AG.
 (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
 WPI; 2000-679374/66.
 Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity
 Disclosure; Page 58-62; 62pp; English.
 A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pNOV1704 comprises the Zea mays ubiquitin promoter, the phosphate mannose isomerase selectable marker and the nopaline synthase termination sequence. pNOV1704 further comprises the Zea mays ubiquitin promoter operably linked to the trichothecene 3-O-acetyl transferase sequence given in GENESEQ record AAAS4206 and the nos termination sequence.
 Sequence 12949 BP; 3194 A; 3146 C; 3143 G; 3466 T; 0 other;
 Query Match 67.5%; Score 915.6; DB 21; Length 12949;
 Best Local Similarity 80.3%; Pred. No. 2.1e-280;
 Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
 3 GGCTTTCAAGATACAGCTCGACACCCCTCGCGCAGCTACCGGCTCTCTTGGATCTACAC 62
 11281 GTCTTTGACATAGAGCTCGACATCATCGGCAGCAACCCGCTCTCTTCAATCTACAC 11340
 63 CCAATCAGTCTCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTGTGAGCAC 122
 11341 CCAGATCAGTCTCTGTTTACCCCGTCTCTGATCCCTCCAGTATCCGACCATCGTACGAC 11400
 123 CTTTCGACCAAGGCTTAAGCGCTTCTCGAAGCGCTGCCATCGGTGCGAGCCAGGTCAA 182
 11401 CTTTGAGGAGGGCTAAAGCGCTCTCTCAAACTTCCATGCGTGGTCCGCGCCAGGTCAA 11460
 183 AGCCGAGGATAGCGAGGAGAACACAGAGAACTTCTTATCGTCCCTTTTGGAGCGT 242
 11461 GACCGGGCATGCGGAGAGAAACACAGGAACCTTCCAAATCATTCATATGAGGAGAC 11520
 243 TCCTCGTGTGTAGTGAAGACCTTCCGCGATGATCTTCAGCGCCACGATCGAGGGTAT 302
 11521 ACCCGTCTGTGTGAAGACCTTCCGATGATCTTCAGCGCCACGATCGAGGGGT 11580
 303 GAGAAAGCGGGATACCTATGCGATGTTTGAAGAGAACATCATCGCGCCAGAGAGAC 362
 11581 GAGAAAGCGGGATTTCCCTTAGAGATGTTTGAAGAGAACCTGCTCGCGAGAGAC 11640
 363 GTTACCTATTGGACCTGGTACTGTCCGAGGACCCAAAGCCTGTAACTTATTTGAGCT 422
 11641 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCTGTGTGCTATTGCACT 11700
 423 CAATCTCATCAAGGGCGGACTCATCTCTCACTGTCAACGGACAGCACGCTGCTATGATAT 482

Db 11701 CAATTTCAITTAAGGGCGGACTCAITTTCTCACCGTCAACGGAACAATGTTGCTATGGACAT 11760
 QY 483 GGTAGGCCAAGANTGGGTGATCCCGTCTACTCTCCAAAGCGTCCCGTAACGACCCATTAC 542
 Db 11761 GACAGGACAAGATGCAATTAATTCGTCTCTCTCCAAAGCGTCCCGCAAGATCATTCAC 11820
 QY 543 CGAGAGAAATGACGGGCATGAACCTCGATCGAAGACGATAGTTCTTTAAGGAA 602
 Db 11821 CGAGGAGAAATCTCGGCCATGAACCTCGATCGAAGACGATAGTTCTTTGAAAA 11880
 QY 603 CTATACGATTGCGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGA 662
 Db 11881 CTACAAAGTTGCTCTGAGCTAGACCACCATCCCAACCC---TGGCGCTGCTGGGGA 11937
 QY 663 CGCTGTTCTACCGCGGTCACTGCAAGCTGGGCGTCTTTTCAATTCACGCCCCCAAGCCAT 722
 Db 11938 CGCTCCACCGCACCGGCCAAGGCAAGCTGGGCGTCTTTTCAATTCACGCCCCCAAGCCCT 11997
 QY 723 GTCAGAGCTCAAGGATGCTCTACCAAGCTCTTGAAGCATCAACAAAGTTGCTGTCAC 782
 Db 11998 CTCGAGCTGAAGACGCGAGCCACAAAGACTCTTGAAGCGTCTTCAAGTTTGTCAAC 12057
 QY 783 TGACGATCTCTTTCGGGTTTCACTGGAATCGGCTCTCGCTGCGTCTCGAAGAT 842
 Db 12058 TGATGATCTCTTTCGGGTTTATCTGCAATCAACCTCGCGGTACGCTCTGCAAGAT 12117
 QY 843 CGATGGCTCTGACCTACCGAGTTCTGCGGTGCTTGTGATGCTCGACCGCAATGGGT 902
 Db 12118 GGATGTTTCCACACTACTGAATTTCTCGCGCTGTGACATGCGGGGCCCAATGGGCT 12177
 QY 903 CTCGAAACACTACCGAGGCTCTTCAAAATGACCTTACCAATCTGACATCGCGGGA 962
 Db 12178 ATCAAGCACATACCCAGGCTCTTCTTCAAAATGACCTTACCAATCTGACATCGCGGGA 12237
 QY 963 AATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCTGTTTCAAGACTCGACCCCGC 1022
 Db 12238 AATCGCAACGACACTTGGCGCAACAGCATCAAGCTTCTGTTTCAAGACTCGACCCGGA 12297
 QY 1023 GAGCATGCGCGAGCAACAGAGGTCTCGGACGTCTCGCAACCTGCTGCAACCAACCCCGCAAGTC 1082
 Db 12298 TCGTTTGGCAGAGCAACACAGCTTTGGCGACGTATCATGATGCGCTCTGACAGTC 12357
 QY 1083 CAAGTATCCCTGACGGCTGATGCGGACCCATCTACAGGCTCATGCTGAGTTCTTGGGC 1142
 Db 12358 GAGCTCTCCCTGACCGCGATGCGAATCCGTCAAGCAGCATCATGCTGAGTTCTTGGGC 12417
 QY 1143 CAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG 1202
 Db 12418 CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAGCCCTGAGAGTGTGAG 12477
 QY 1203 AGCGCCAAATCTTTGAGCTCTGAGAGCTTTGATGATCTTTATGCCCAAGAGCCCTGATGG 1262
 Db 12478 AAGACCTCGCTTTGAACCTTTTGAAGTCTTATGAGAGTTTGAAGTCTTTATGCCCAAGAGCCCTGATGG 12537
 QY 1263 CGAGTCTGTGGGCGCTTTCTCTGAGGATGAGGATATGAGACGATGAGAGCGGATAA 1322
 Db 12538 GGAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGCGGATGA 12597
 QY 1323 GGAGTGACCAAGTATGCGGAGTACCTGCTTAG 1356
 Db 12598 GGAGTGACCAAGTATGCGCAAAAGTATATTGGGTAG 12631

RESULT 5
 AAAS4212
 ID AAAS4212 standard; DNA; 13737 BP.
 XX
 AC AAAS4212;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Transformation vector pAgroIR.
 XX

QY	1312	AAGCGGATAGGAGTGGACCAAGTATGC	1340	Matches	325;	Conservative	0;	Mismatches	225;	Indels	15;	Gaps	3;
DB	1381	AATGCGGATAAAGATGGACAAATATGC	1409										
RESULT 7													
ID	AAFL12071	standard; cDNA; 695 BP.											
AC	AAFL12071;												
DT	13-MAR-2001	(first entry)											
DE	Aspergillus oryzae	EST SEQ ID NO:4594.											
XX	Multiple gene expression; filamentous fungal cell; EST;												
KW	expressed sequence tag; Fusarium venenatum; Aspergillus niger;												
KW	Aspergillus oryzae; Trichoderma reesei; identification; recombination;												
KW	culture condition; environmental stress; spore morphogenesis;												
KW	metabolic pathway engineering; catabolic pathway engineering; ss.												
XX	Aspergillus oryzae.												
OS	WO2000056762-A2.												
PN	28-SEP-2000.												
PD	22-MAR-2000; 2000WO-US07781.												
XX	22-MAR-1999; 99US-0273623.												
PR	(NOVO) NOVO NORDISK BIOTECH INC.												
PA	(NOVO) NOVO NORDISK AS.												
XX	Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;												
PI	WPI; 2000-594572/56.												
XX	Monitoring differential expression of genes in filamentous fungal cells												
PT	uses fluorescence-labeled nucleic acids isolated from the cells and a												
PT	substrate of expressed sequence tags -												
XX	Claim 88; Page 1954-1955; 3161pp; English.												

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organization of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.

Sequence 695 BP; 174 A; 191 C; 156 G; 172 T; 2 other;

Query Match 10.8%; Score 146.2; DB 21; Length 695;
Best Local Similarity 57.5%; Pred. No. 8.9e-36;

RESULT 8

ABZ54817	ID	ABZ54817	standard; cDNA; 482 BP.
XX	AC	ABZ54817;	
XX	DT	28-MAR-2003	(first entry)
XX	DE	Aspergillus oryzae	polynucleotide SEQ ID NO 3930.
XX	XX	Aspergillus oryzae;	fermentation; fungus; industrial; EST;
XX	KW	expressed sequence tag; gene; ss.	
XX	OS	Aspergillus oryzae.	
XX	FN	WO200279476-A1.	
XX	PD	10-OCT-2002.	
XX	PF	22-MAR-2002; 2002WO-IB00890.	
XX	PR	30-MAR-2001; 2001JP-0098371.	
XX	PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.	
XX	PA	(NARE-) NAT RES INST BREWING.	
XX	PA	(NORQ) NAT FOOD RES INST MIN AGRIC.	
XX	XX	Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;	
XX	PI	Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;	
XX	XX		


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PR 24-JUN-1998; 98US-0103840.
XX (GENO-) INST GENOMIC RES.
XX Fleischmann RD, White OR, Fraser CM, Venter JC;
XX WPI; 2001-647261/74.
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
XX determining the nucleotide sequence of the strain at positions in the
XX genome corresponding to positions where M. tuberculosis strains CDC
XX 1551 and H37Rv differ
XX
XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
XX different populations of the tuberculosis bacterial pathogen,
XX Mycobacterium tuberculosis or related Mycobacterium by determining the
XX nucleotide sequence of the first strain at positions in the complete
XX sequence of the genome that correspond to positions that differ in the
XX nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
XX H37Rv (AAI99682). The method is useful for evaluating strain variation of
XX M. tuberculosis and has valuable application in the fields of
XX tuberculosis genetics, epidemiology, patient treatment and epidemic
XX monitoring.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?docID=629432851.
XX
XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
SQ
Query Match 2.9%; Score 39.8; DB 22; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 8.4;
Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
QY 956 TCGGCGAAATCGCAAGTCACTCGGCGCAACAGCATCAGCGCTTCGTTCAAGACTCG 1015
DB 4227170 TCGAGAGGTTTCGGCGGCCCACTCGACGAAGCAGCGCAATCGCGATATCC 4227229
QY 1016 ACCCGCGAGATCGCGCAGCAAGAGGTCTCGGAGCTACTCTCACACACCCCG 1075
DB 4227230 ACGCCACAGCATCCGCGAACTCGAAGATGCTCTGCGCCCGGAACCTCGCGAGGAGTCG 4227289
QY 1076 ACGAGTCCACGATATCCCTGACGCTGATCGGACCCATCTACAGGCTCATGCTGAGTT 1135
DB 4227290 ACCGGTTACCTGCGCTTCAAGAGACGCGCTCGGACCGCGAGTTGCGCATG 4227349
QY 1136 CTTGGGCGAAGTGGGACTCTGG 1158
DB 4227350 CCCAGGCACAGCTGTCGGCTGG 4227372
RESULT 11
AAT37310
ID AAT37310 standard; cDNA to mRNA; 1605 BP.
XX AAT37310;
XX
XX 06-FEB-1997 (first entry)
XX
XX Aromatic acyl transferase coding sequence.
XX
XX Aromatic acyl transferase; transformation; anthocyanin pigment;
XX plants; acylation; colour; tone; colouration; colour change;
XX Gentiana triflora; Petunia hybrida; Perilla ochroides;
XX Scenecio cruentus; Lavandula angustifolia; ds.
XX
XX Petunia hybrida (Clone pPAT48).
XX
XX Key Location/Qualifiers
FH 67..1413
FT CDS /*tag= a
FT /product= Aromatic acyl transferase.
```

```
XX WO9625500-A1.
XX
XX 22-AUG-1996.
XX
XX 16-FEB-1996; 96WO-JP00348.
XX
XX 30-JAN-1996; 96JP-0046534.
XX 17-FEB-1995; 95JP-0067159.
XX 29-JUN-1995; 95JP-0196915.
XX (SUNR ) SUNTORY LTD.
XX
XX Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
XX Nakao M, Tanaka Y, Yonekura K;
XX WPI; 1996-393401/39.
XX P-PSDB; AAM04724.
XX
XX DNA coding for aromatic acyl transferase - for transforming plants
XX which produce anthocyanin pigments and thus altering colour tone,
XX e.g. of flowers
XX
XX Claim 4; Page 61-65; 94pp; Japanese.
XX
XX Vectors containing DNA fragments encoding proteins of plant origin
XX with aromatic acyl transferase activity may be used to transform
XX plants which produce anthocyanin pigments. The aromatic acyl
XX transferase acylates the pigments in the flower resulting in colour
XX tone changes and allowing new colourations to be produced. Six
XX specific DNA sequences encoding aromatic acyl transferase from
XX different plants are described in AAT37308-T37313.
XX
XX Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 other;
SQ
Query Match 2.7%; Score 36.4; DB 17; Length 1605;
Best Local Similarity 51.9%; Pred. No. 1.4;
Matches 107; Conservative 0; Mismatches 96; Indels 3; Gaps 1;
QY 1154 TCTGGGATTACGACTTTGGCTCGGACTGGGTAAAGCCCGGAGCTGTGAGACGGCCAAATCT 1213
DB 1217 TCAAGGTTTACGACGTGATTTGGATGGGGAAGCCAGAGAGTGTGAGGAGTGTGGA 1276
QY 1214 TTGAGCCCTGTGAGAGCTTGATGTACTTTATGC--CCAAGAGCCCTGATGCGGAGTTCT 1270
DB 1277 ACAATAGTGTGATGGAATGGTGATTTGTACCAAGGCAAAATGGAGGAAGAGCAATTG 1336
QY 1271 GTGCGGCGCTTCTCTGAGGAGTGAAGATATGACCGATTCAGCGCGGTAAGAGGTGGA 1330
DB 1337 ATGTGGAGATTAGTTTGGAAAGCAATGCTATGGAGAGGTTGGAGAAAGATAAGAGTTCC 1396
QY 1331 CCAAGTATGCGCAGTACGTTGTTAG 1356
DB 1397 TCATGGAACCTGCTTAATTGCTTAG 1422
RESULT 12
ABQ33692/c
ID ABQ33692 standard; DNA; 1459 BP.
XX ABQ33692;
XX
XX 12-JUL-2002 (first entry)
XX
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 20283.
XX
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX
XX OS
```


PN W0200218632-A2.
XX PD 07-MAR-2002.
XX PF 01-SEP-2001; 2001WO-BP10074.
XX PR 01-SEP-2000; 2000DE-1043826.
XX PR 05-SEP-2000; 2000DE-1044543.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX DR WPI; 2002-371829/40.
XX PT Determining the degree of cytosine methylation in genomic DNA, useful
XX PT amplicons from chemically treated DNA -
XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX CC This invention describes a novel method for determining the degree of
XX CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX CC genomic sample of DNA. The sample is treated chemically to convert
XX CC cytosine (C) but not methylated C, to uracil, then part of the genomic
XX CC DNA that contains the target C is amplified to form a labeled amplicon.
XX CC The amplicon is hybridised to two classes, each with at least one
XX CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX CC and the degree of hybridisation to both classes is determined from the
XX CC label on the amplicon. From the ratio of labels hybridised to the two
XX CC classes of oligomers, the degree of methylation is calculated. The method
XX CC is used: (i) for diagnosis and/or prognosis of side effects of
XX CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX CC of the central nervous, cardiovascular, gastrointestinal and respiratory
XX CC systems etc., particularly by detecting mutations or single nucleotide
XX CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX CC types and for investigating cell differentiation. The method allows the
XX CC methylation status of many C residues to be determined simultaneously.
XX CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the
XX CC method for determining the degree of cytosine methylation described in
XX CC the disclosure of the invention.
XX SQ Sequence 1459 BP; 173 A; 200 C; 526 G; 560 T; 0 other;
Query Match 2.6%; Score 35.6; DB 24; Length 1459;
Best Local Similarity 49.0%; Pred. No. 2.4;
Matches 95; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 21 CGACACCTCGGCCAGCTTACCGAGGCTCTTTCGATCTACACCCCAATCAGTCTCTCTA 80
Db 1108 CCAATTCGCGCCCACTCCGACCCGCTTACACCCGCGCCCGAGCAATCCCAAC 1049
Qy 81 CCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAGGCTCTTAA 140
Db 1048 CACCGCGCGTAAACGACCAAAATTAATCTCTACCCGCGCTTTAAACCCGAAACGCA 989
Qy 141 GCGCTTCTCGAAGCGCTCCCATGGTTCGAGGCGAGGTCAAAGCGGAGGCGATTAGCGA 200
Db 988 ACGAATCGAACCAACCCGAAACGCGCGTCTTCGCGAATCTTAAACACGACGAATCGACGA 929
Qy 201 GGGAAACACAGGAA 214
Db 928 CCGAAAAAACGAA 915
RESULT 13
ID ABQ33693
XX ABQ33693 standard; DNA; 1459 BP.
AC ABQ33693;
XX 12-JUL-2002 (first entry)
XX DT
XX

DE XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 20284.
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
OS Homo sapiens.
XX XX W0200218632-A2.
PN PD 07-MAR-2002.
XX PF 01-SEP-2001; 2001WO-BP10074.
XX PR 01-SEP-2000; 2000DE-1043826.
XX PR 05-SEP-2000; 2000DE-1044543.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX DR WPI; 2002-371829/40.
XX PT Determining the degree of cytosine methylation in genomic DNA, useful
XX PT for diagnosis and prognosis, comprises selective hybridization of
XX PT amplicons from chemically treated DNA -
XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX CC This invention describes a novel method for determining the degree of
XX CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX CC genomic sample of DNA. The sample is treated chemically to convert
XX CC cytosine (C) but not methylated C, to uracil, then part of the genomic
XX CC DNA that contains the target C is amplified to form a labeled amplicon.
XX CC The amplicon is hybridised to two classes, each with at least one
XX CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
XX CC and the degree of hybridisation to both classes is determined from the
XX CC label on the amplicon. From the ratio of labels hybridised to the two
XX CC classes of oligomers, the degree of methylation is calculated. The method
XX CC is used: (i) for diagnosis and/or prognosis of side effects of
XX CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
XX CC of the central nervous, cardiovascular, gastrointestinal and respiratory
XX CC systems etc., particularly by detecting mutations or single nucleotide
XX CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
XX CC types and for investigating cell differentiation. The method allows the
XX CC methylation status of many C residues to be determined simultaneously.
XX CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the
XX CC method for determining the degree of cytosine methylation described in
XX CC the disclosure of the invention.
XX SQ Sequence 1459 BP; 560 A; 526 C; 200 G; 173 T; 0 other;
Query Match 2.6%; Score 35.6; DB 24; Length 1459;
Best Local Similarity 49.0%; Pred. No. 2.4;
Matches 95; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 21 CGACACCTCGGCCAGCTTACCGAGGCTCTTTCGATCTACACCCCAATCAGTCTCTCTA 80
Db 352 CCAATTCGCGCCCACTCCGACCCGCTTACACCCGCGCCCGAGCAATCCCAAC 411
Qy 81 CCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAGGCTCTTAA 140
Db 412 CACCGCGCGTAAACGACCAAAATTAATCTCTACCCGCGCTTTAAACCCGAAACGCA 471
Qy 141 GCGCTTCTCGAAGCGCTCCCATGGTTCGAGGCGAGGTCAAAGCGGAGGCGATTAGCGA 200
Db 472 ACGAATCGAACCAACCCGAAACGCGCGTCTTCGCGAATCTTAAACACGACGAATCGACGA 531
Qy 201 GGGAAACACAGGAA 214
Db 532 CCGAAAAAACGAA 545

```

RESULT 14
ABQ14442/c
ID ABQ14442 standard; DNA; 1463 BP.
XX
AC ABQ14442;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1033.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1463 BP; 189 A; 200 C; 521 G; 553 T; 0 other;
XX
Query Match 2.6%; Score 35.6; DB 24; Length 1463;
Best Local Similarity 49.0%; Pred. No. 2.4;
Matches 95; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
XX
QY 21 CGACACCTCGCCAGCTACAGGCTCTTTTCGATCTACACCCAAATCAGTCTCTCTTA 80
DB 1018 CCAATTGCGGCCCACTCCGACCCACGTTTACCCCGCCCGCAGCAATCCCCAC 959
QY -81 CCCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGACCTTCGAGCAAGTCTTAA 140
DB 958 CACCGCGCGTAAACGACCAAAATTAATCTCTACCCCGCGGTTTAAAAACCGAACGCA 899

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QY 141 GCGCTTCTCGAAGCCGTCCTCCATGGTCCGACGCCAGGTCAAGCCGAGGCATTAGCGA 200
DB 898 ACGAATCGAACACCCGAAACCGCGTCTTCCGCGAATCTTAAAAACGACGAATCGACGA 839
QY 201 GGGAAACACAGGAA 214
DB 838 CCGAAAAAACAAGAA 825
XX
RESULT 15
ABQ14443
ID ABQ14443 standard; DNA; 1463 BP.
XX
AC ABQ14443;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 1034.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 1463 BP; 553 A; 521 C; 200 G; 189 T; 0 other;
XX
Query Match 2.6%; Score 35.6; DB 24; Length 1463;
Best Local Similarity 49.0%; Pred. No. 2.4;

```

Matches	95;	Conservative	0;	Mismatches	99;	Indels	0;	Gaps	0;
Qy	21	CGACACCTCGCGCCAGCTACGAGGCTCTTTTCGATCTACACCCAAATCAGTCTCTCTTA	80						
Db	446	CAAAATTCGCGCCCAACTCCGACCCCGAGTTTACACCCCGCCCGACGAATCCGCACAC	505						
Qy	81	CCCCGTCTCTGANTCTCTCAATATCCCACTATTGTGACACCTTCGAGCRAAGTCTTAA	140						
Db	506	CACCGCGGTAAACGACCAAAATTAATCTCTACCCCGGCTTTAAACCCGAAACGCA	565						
Qy	141	GCGTTTTCGGAAGCGTCCATGGTTCGAGGCCAGGTCAAAGCCGAGGGCATTAGGGA	200						
Db	566	ACGAATCGAACAACCCGAAACGCGGTCTTCCGCGAATCTTAAACGACGHAATCGACGA	625						
Qy	201	GGGAACACAGGAA	214						
Db	626	CGAAAAAAACGAA	639						

Search completed: February 7, 2004, 21:53:45
Job time : 417 secs

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 17:54:07 : Search time 5222 Seconds
(without alignments)
10623.028 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacagct.....atggcagtaagtgtgtag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1356	100.0	1356	6	AR193433	AR193433 Sequence
2	1340	98.8	1605	8	E31785	E31785 Trichothec
3	1340	98.8	1605	8	AB000874	AB000874 Gibberell
4	1340	98.8	3003	8	AB009607	AB009607 Gibberell
5	1340	98.8	8646	8	AB011417	AB011417 Gibberell
6	1334	98.4	1336	8	AF212605	AF212605 Gibberell
7	1334	98.4	1336	8	AF212608	AF212608 Gibberell
8	1330.8	98.1	1336	8	AF212603	AF212603 Gibberell
9	1330.8	98.1	1336	8	AF212606	AF212606 Gibberell
10	1330.8	98.1	1336	8	AF212607	AF212607 Gibberell
11	1329.2	98.0	1336	8	AF212602	AF212602 Gibberell
12	1329.2	98.0	1336	8	AF212604	AF212604 Gibberell
13	1321.2	97.4	1336	8	AF212582	AF212582 Gibberell
14	1321.2	97.4	1336	8	AF212583	AF212583 Gibberell
15	1321.2	97.4	1336	8	AF212584	AF212584 Gibberell
16	1321.2	97.4	1336	8	AF212585	AF212585 Gibberell
17	1321.2	97.4	1336	8	AF212586	AF212586 Gibberell
18	1321.2	97.4	1336	8	AF212587	AF212587 Gibberell
19	1319.6	97.3	1336	8	AF212594	AF212594 Gibberell
20	1319.6	97.3	1336	8	AF212601	AF212601 Gibberell
21	1318	97.2	1336	8	AF212595	AF212595 Gibberell
22	1318	97.2	1336	8	AF212596	AF212596 Gibberell
23	1318	97.2	1336	8	AF212597	AF212597 Gibberell
24	1318	97.2	1336	8	AF212598	AF212598 Gibberell
25	1318	97.2	1336	8	AF212599	AF212599 Gibberell
26	1318	97.2	1336	8	AF212600	AF212600 Gibberell
27	1316.4	97.1	1336	8	AF212588	AF212588 Gibberell
28	1314.8	97.0	1336	8	AF212589	AF212589 Gibberell
29	1304.4	96.2	1322	8	AY222642	AY222642 Gibberell
30	1304.4	96.2	1322	8	AY225882	AY225882 Gibberell
31	1303.6	96.1	1336	8	AF212590	AF212590 Gibberell
32	1303.6	96.1	1336	8	AF212591	AF212591 Gibberell
33	1303.6	96.1	1336	8	AF212592	AF212592 Gibberell
34	1303.6	96.1	1336	8	AF212593	AF212593 Gibberell
35	1287.6	95.0	1336	8	AF212614	AF212614 Fusarium
36	1284.4	94.7	1336	8	AF212612	AF212612 Fusarium
37	1282.8	94.6	1336	8	AF212613	AF212613 Fusarium
38	1281.2	94.5	1336	8	AF212611	AF212611 Fusarium
39	1271.6	93.8	1336	8	AF212609	AF212609 Fusarium
40	1270	93.7	1336	8	AF212610	AF212610 Fusarium
41	1247.6	92.0	1336	8	AF212615	AF212615 Fusarium
42	1247.6	92.0	1336	8	AF212616	AF212616 Fusarium
43	1247.6	92.0	1336	8	AF212617	AF212617 Fusarium
44	1247.6	92.0	1336	8	AF212618	AF212618 Fusarium
45	915.6	67.5	1403	6	AR193430	AR193430 Sequence

ALIGNMENTS

RESULT 1
AR193433
LOCUS AR193433 1356 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5 from patent US 6346655.
ACCESSION AR193433
VERSION AR193433.1 GI:20239398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmemon,J.
TITLE Trichothec-Resistant transgenic plants
JOURNAL Patent: US 6346655-A 5 12-FEB-2002;
FEATURES Location/Qualifiers

source		1. .1356					
BASE COUNT		319 a 385 c 349 g		303 t			
ORIGIN							
Query Match		100.0%; Score 1356; DB 6; Length 1356;					
Best Local Similarity		100.0%; Pred. No. 0;					
Matches 1356; Conservative		0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGGCTTTCAAGATACAGCTCGACACCCCTGGCCAGCTACAGGCTCTCTTCGATCTAC	60				
DB	1	ATGGCTTTCAAGATACAGCTCGACACCCCTGGCCAGCTACAGGCTCTCTTCGATCTAC	60				
QY	61	ACCAAAATCAGTCTCTTACCCCGTCTCTGATCTCTCAATATCCCATATTTGTCAGC	120				
DB	61	ACCAAAATCAGTCTCTTACCCCGTCTCTGATCTCTCAATATCCCATATTTGTCAGC	120				
QY	121	ACCTTCGAGCAAGGCTTTAAGCGCTTCTCGAAGCCGTCCTCATGGGTGCGAGGCCAGGTC	180				
DB	121	ACCTTCGAGCAAGGCTTTAAGCGCTTCTCGAAGCCGTCCTCATGGGTGCGAGGCCAGGTC	180				
QY	181	AAAGCCGAGGGCAATTAGCGAGGAAACACAGGAATCTCTTTATCGTCCCTTTTGGAGC	240				
DB	181	AAAGCCGAGGGCAATTAGCGAGGAAACACAGGAATCTCTTTATCGTCCCTTTTGGAGC	240				
QY	241	GTTCCTCGTGTGTAGTGAAGACCTCGCGATGATCCTTCAGCGCCACGATCGAGGGT	300				
DB	241	GTTCCTCGTGTGTAGTGAAGACCTCGCGATGATCCTTCAGCGCCACGATCGAGGGT	300				
QY	301	ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAAGGAAG	360				
DB	301	ATGAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAAGGAAG	360				
QY	361	ACGTTACTATTGGACCTGTACTGTGTCGAGACCCAAAGCTGTAATCTTATTCGAG	420				
DB	361	ACGTTACTATTGGACCTGTACTGTGTCGAGACCCAAAGCTGTAATCTTATTCGAG	420				
QY	421	CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAACGACAGCAGGTGTATGGAT	480				
DB	421	CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAACGACAGCAGGTGTATGGAT	480				
QY	481	ATGTGAGGCAAGATGGGTGATCCGCTACTCTCCAAAGCGGTGCCGTAAACGCCATTC	540				
DB	481	ATGTGAGGCAAGATGGGTGATCCGCTACTCTCCAAAGCGGTGCCGTAAACGCCATTC	540				
QY	541	ACCGAAGAGGAATGACGGCCATGAACTCTGATCGAAGACGATAGTTCCTTACCTTGAA	600				
DB	541	ACCGAAGAGGAATGACGGCCATGAACTCTGATCGAAGACGATAGTTCCTTACCTTGAA	600				
QY	601	AACTATAGATTGGCCCGGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGGTGGT	660				
DB	601	AACTATAGATTGGCCCGGAGGTAGATCATCAGATTGTCAAGCTGATGTAGCTGGTGGT	660				
QY	661	GACGCTGTTCTCAGCGCGGTCAAGTCAAGCTGGCGTCTTTCACATTCAGCCCCAAGGCC	720				
DB	661	GACGCTGTTCTCAGCGCGGTCAAGTCAAGCTGGCGTCTTTCACATTCAGCCCCAAGGCC	720				
QY	721	ATGTCAGAGCTCAAGGATGTGCTACCAAGACTCTTGACGATCAACAAAGTTCGTGTGCG	780				
DB	721	ATGTCAGAGCTCAAGGATGTGCTACCAAGACTCTTGACGATCAACAAAGTTCGTGTGCG	780				
QY	781	ACTGACATGCTCTTTCGGCGGTTCATCTGGAAATCGGCTCTCGGTGCGTCTCGAAAGA	840				
DB	781	ACTGACATGCTCTTTCGGCGGTTCATCTGGAAATCGGCTCTCGGTGCGTCTCGAAAGA	840				
QY	841	ATCGATGGCTCTGCACTTACCGAGTCTTCCGCTGTGTTGATGCTCGACCGCAATGGGT	900				
DB	841	ATCGATGGCTCTGCACTTACCGAGTCTTCCGCTGTGTTGATGCTCGACCGCAATGGGT	900				
QY	901	GTCTCGAAACAATACCCAGGCTTCTTCAAAACATGACTTACCAACTTCGACCATCGGC	960				
DB	901	GTCTCGAAACAATACCCAGGCTTCTTCAAAACATGACTTACCAACTTCGACCATCGGC	960				

QY	961	GAATTCGCCAACAGGTCTCTGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCCGACCC	1020				
DB	961	GAATTCGCCAACAGGTCTCTGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCCGACCC	1020				
QY	1021	GGCAGCATCGCCAGCGAAACAAGAGTCTTCGCGAGTACTCTGCAACAACACCCGACAAG	1080				
DB	1021	GGCAGCATCGCCAGCGAAACAAGAGTCTTCGCGAGTACTCTGCAACAACACCCGACAAG	1080				
QY	1081	TCCAACGATATCCCTGACGGCTGATCGGACCCATCTACGAGGTATGCTGAGTTCCTTGG	1140				
DB	1081	TCCAACGATATCCCTGACGGCTGATCGGACCCATCTACGAGGTATGCTGAGTTCCTTGG	1140				
QY	1141	GCACAAGTCTGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGTAAAGCCGAGACTGTG	1200				
DB	1141	GCACAAGTCTGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGTAAAGCCGAGACTGTG	1200				
QY	1201	AGACGGCCCAATCTTTGAGCCTCTTGAGACTTTGATGTACTTTATGCCCAGAAGCCTGAT	1260				
DB	1201	AGACGGCCCAATCTTTGAGCCTCTTGAGACTTTGATGTACTTTATGCCCAGAAGCCTGAT	1260				
QY	1261	GGCGAGTTCTGTGCGCGCTTTCTCTGAGGGATGAGGATATGACCGATTGAAGCGGAT	1320				
DB	1261	GGCGAGTTCTGTGCGCGCTTTCTCTGAGGGATGAGGATATGACCGATTGAAGCGGAT	1320				
QY	1321	AAGGAGTGGACCAAGATATGCGAGTACGTTGGTTAG	1356				
DB	1321	AAGGAGTGGACCAAGATATGCGAGTACGTTGGTTAG	1356				

RESULT 2	E31785	1605 bp	DNA	linear	PAT 18-JUN-2001	
LOCUS	Trichothecene 3-O-acetyltransferase gene.					
DEFINITION	E31785					
ACCESSION	E31785.1					
VERSION	GI:13018619					
KEYWORDS	JP 2000032985-A/1.					
SOURCE	Gibberella zeae					
ORGANISM	Gibberella zeae					
REFERENCE	1 (bases 1 to 1605)					
AUTHORS	Iseami, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.					
TITLE	Trichothecene 3-O-acetyltransferase gene					
JOURNAL	Patent: JP 2000032985-A 1 02-FEB-2000;					
COMMENT	RIKAGAKU KENKYUSHO, ISAMU YAMAGUCHI					
OS	Fusarium graminearum					
PN	JP 2000032985-A/1					
PD	02-FEB-2000					
PF	15-JUL-1998 JP 1998200280					
PI	ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI KOSHINO, PI KATSUMI YONEYAMA					
PC	C12N15/09, A01H5/00, A01N63/00, C12N1/21, C12N5/10, C12N9/10// PC (C12N15/09, C12R1:77), (C12N1/21, C12R1:19), (C12N5/10, C12R1:91), PC C12N15/00,					
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FT	CDS 135..1487.					
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Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;						
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Db 255 ACCTTCGAGCAAGGTCTTAAGCGCTCTCTCCGAGCGCTGCCATGGGTCCGACGCCAGAGTC 314
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QY 241 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTTCAGCGCCACGATCGAGGT 300
Db 375 GTTCTCTGTTGTAGTGAAGACCTCCGCGATGATCTTTCAGCGCCACGATCGAGGT 434
QY 301 ATGAGAAAGCGGGGATACCTTATGGCGATGTTTGGAGAGAACATCATCGCGCAAGGAAG 360
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QY 361 AGTTTACCTATTGGACCTGTTACTGTTCCGAGACGCCAAAGCCTGTATTTCTATTGCGAG 420
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QY 421 CTCAACTTTCATCAAGCGCGGACTCATCTCTCACTGTCAAGGACGACACGCTGTATGAT 480
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Db 675 ACCGAGAGGAAATGACGGCGATGAACTCTGATCGCAAGACGATAGTTTCTTACCTTGAA 734
QY 601 AACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAGCTGATGATGCTGGT 660
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QY 661 GACGTGTCTTCAGCGCGGTGATGCAAGCTGCGGCTTCTTCAATTCAGCGCCCAAGGCC 720
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QY 781 ACTGACGATGCTCTTTCGCGGTTTCATCTGGAATCGGCTCTCGGTGCGTCTCGAAGA 840
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QY 1021 GCGAGCATGCGCCAGCAAGAGGTCTCGCAGCTACCTGCAACACACACCCGACAAG 1080
Db 1155 GCGAGCATGCGCCAGCAAGAGGTCTCGCAGCTACCTGCAACACACACCCGACAAG 1214
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QY 1141 GCGAAGTGGGACTCTGGGATTAACGATTTGGCTCGGACTGGTAAGCCCGAGACTGTG 1200
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QY 1201 AGACGCCCAATCTTTGAGCGCTTTCAGAGCTTGATGATCTTTATGCCCAAGAGCCTGAT 1260
Db 1335 AGACGCCCAATCTTTGAGCGCTTTCAGAGCTTGATGATCTTTATGCCCAAGAGCCTGAT 1394
QY 1261 GCGGAGTTCTGTGCGCGCTTTCTCTGAGGGATGAGGATATGACGATTTGAAGCGGAT 1320
Db 1395 GCGGAGTTCTGTGCGCGCTTTCTCTGAGGGATGAGGATATGACGATTTGAAGCGGAT 1454
QY 1321 AAGGAGTGGAACCAAGTATGCGCAGTACGTTGGTTAG 1356
Db 1455 AAGGAGTGGAACCAAGTATGCGCAGTACGTTGGTTAG 1490

RESULT 3
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DEFINITION
AB000874
ACCESSION
VERSION
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BASE COUNT 397 a 459 c 393 g 356 t
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Query Match 98.8%; Score 1340; DB 8; Length 1605;

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complete cds.
1605 bp mRNA linear PLN 21-JAN-1998
AB000874
AB000874.1 GI:2804249
trichothecene 3-O-acetyltransferase.
Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (sites)
Kimura, M., Kaneko, I., Komiyama, M., Takatsuki, A., Koshino, H.,
Yoneyama, K. and Yamaguchi, I.
Trichothecene 3-O-acetyltransferase protects both the producing
organism and transformed yeast from related mycotoxins. Cloning and
characterization of Tril101
J. Biol. Chem. 273 (3), 1654-1661 (1998)
98104153
9430709
2 (bases 1 to 1605)
Kimura, M.
Direct Submission
Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hirosewa 2-1, Wako, Saitama 351-01, Japan
(E-mail: mkimura@postman.riken.go.jp, Tel: 81-048-467-9518,
Fax: 81-048-462-4676)
Location/Qualifiers
1. .1605
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 61 ACCCAATCAGTCTCTTACCCCGTCTGTGATCTCTCAATATCCCACTATTGTCAGC 120
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QY 121 ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCGAAGCCGTCCCATGGTTCGAGCCAGGTC 180
DB 255 ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCGAAGCCGTCCCATGGTTCGAGCCAGGTC 314

QY 181 AAGCCGAGGGCAATAGCGAGGAAACACAGGAATCTTCTTTATCGTCCCTTTTGAAGAC 240
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QY 301 ATGAGAAAGCGGGATACCTATGGGATGTTTGACGAGAACATCATCGCGCCAAAGGAG 360
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QY 361 ACGTACCTATTGGACCTGTGATCGGACGACCCAAAGCTGTGATCTATTTCAG 420
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DB 735 AACTATACGATGCGCCGAGTGAATCATCATGTTGTCAGGCTGATGATGCTGTTGGT 794

QY 661 GACGCTGTTCTCAGCGCGGTGAGTGAAGCTGGGCTTCTTCAATTCAGCCCAAGGCC 720
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QY 721 ATGTACAGCTCAAGATGCTGCTCAAGACTCTTTCGAGCTGATGATGCTGCTGTCG 780
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QY 781 ACTGACGATGCTCTTTCGGGCTCATCTGAAATCGGCTCTCGGCTGCTCGAAGA 840
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QY 841 ATCGATGCTCTGACCTACCGAGTCTCTGCGGTGCTGTTGATGCTCGACCGCAATGGT 900
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QY 901 GTCTCGAACAATACCGAGGCTTCTTCAAAACATGACCTACCAACTCGACCATCGGC 960
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QY 961 GAAATCGCAACGAGTCACTCGCGCAACAGCATCAGCGCTTCTGTTCAAGCTCGACCC 1020
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RESULT 4
AB009607 3003 bp DNA linear PLN 25-DEC-2002
LOCUS
DEFINITION
Gibberella zeae genes for UTP-ammonia ligase and trichothecene
3-O-acetyltransferase, partial and complete cds.
ACCESSION
AB009607
VERSION
Tril101; GI:3252781
KEYWORDS
Gibberella zeae
SOURCE
Gibberella zeae
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE
1 Kimura, M., Shingu, Y., Yoneyama, K. and Yamaguchi, I.
Features of Tril101, the trichothecene 3-O-acetyltransferase gene,
related to the self-defense mechanism in *Fusarium graminearum*
Biosci. Biotechnol. Biochem. 62 (5), 1033-1036 (1998)
98312047
PUBMED
9648241
REFERENCE
2 (bases 1 to 3003)
Kimura, M.
Direct Submission
Submitted (06-DEC-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hirose 2-1, Wako, Saitama 351-0198, Japan
(E-mail: mkimura@postman.riken.go.jp, Tel:81-48-467-9518,
Fax:81-48-462-4676)
Location/Qualifiers

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RESULT 6
AF212605
LOCUS
DEFINITION
Gibberella zeae strain NRRL28063 trichothece
3-O-acetyltransferase, partial cds.
ACCESSION
AF212605
VERSION
AF212605.1 GI:12003706
KEYWORDS
SOURCE
ORGANISM
Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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BASE COUNT 317 a 382 c 341 g 296 t
ORIGIN

Query Match 98.4%; Score 1334; DB 8; Length 1336;
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Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ACCTTCGAGCAAGTCTTAAGCGCTTCTCCGAGCGCTTCCATCGGTCGAGCGCCAGGTC 180

123 ACCTTGAGCAAGGCTTTAAGCGCTTCTCGAAGCGCTCCCATGGTCCGAGCCAGGTC 182
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Db 183 AAAGCCGAGGGCATTTAGCGAGGAAACACAGAACTTCCCTTTATCGTCCCTTTGAGGAC 242
QY 241 GTTCTCGTGTGTAGTGAAGACCTTCGCGCATGATCTTCAGCGCCCAAGTCCAGGCT 300
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Db 303 ATGAGAAAGCGGGATACCTATGCGGATGTTGAGGAGAACATCATCGGCCAAGGAAG 362
QY 361 ACGTTACCTATTGGACCTGGTACTCGTCCGAGACCCAAAGCCCTGTAATTCATTGCGAG 420
Db 363 ACGTTACCTATTGGACCTGGTACTCGTCCGAGACCCAAAGCCCTGTAATTCATTGCGAG 422
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Db 843 ATCGATGGCTTCGACCTACCGAGTTCTGCGGCTGCTGTGATGCTCGACCGCAATGGT 902
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LOCUS   AF212603 1336 bp DNA linear PLN 26-JUN-2001
DEFINITION
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3-O-acetyltransferase, partial cds.
ACCESSION
AF212603
VERSION
AF212603.1. GI:12003702
KEYWORDS
Gibberella zeae
SOURCE
Gibberella zeae
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Take, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
PUBMED 10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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BASE COUNT 318 a 383 c 339 g 296 t
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Query Match 98.1%; Score 1330.8; DB 8; Length 1336;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGGCTTTCAAGATACAGCTCGACACCTCGCGCAGCTTACCAGGCTCTCTTTTCGATCTAC 60
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Qy      841 ATCGATGGCTCTGCAACCTTACCGAGTCTGCGGTGTGTGATGCTCGACCGGCAATGGGT 900
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RESULT 9
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LOCUS Gibberella zeae strain NRRL28336 trichothecene
DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212606
VERSION AF212606.1 GI:12003708

KEYWORDS
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
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JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
PUBMED 10869425

REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-UGDA, 1815 N. University St., Peoria, IL 61604, USA

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BASE COUNT 318 a 383 c 339 g 296 t
ORIGIN

Query Match 98.1%; Score 1330.8; DB 8; Length 1336;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGAGGCTCTTTTCGATCTAC 60
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RESULT 10
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LOCUS
DEFINITION
Gibberella zeae strain NR128439 trichothecene
3-O-acetyltransferase, partial cds.
ACCESSION
AF212607
VERSION
AF212607.1 GI:12003710
KEYWORDS
SOURCE
ORGANISM
Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
PUBMED
10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Query Match 98.1%; Score 1330.8; DB 8; Length 1336;
Best Local Similarity 99.9%; Pred. No. 0;
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QY 1 ATGCGTTTCAAGATACAGCTCGACACCTCGCGCCAGCTTACCAGCGCTCTCTTCGATCTAC 60
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RESULT 11
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3-O-acetyltransferase, partial cds.
ACCESSION
AF212602
VERSION
AF212602.1 GI:12003700
KEYWORDS
Gibberella zeae
SOURCE
Gibberella zeae
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
PUBMED
10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
JOURNAL
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ACCESSION AF212604
VERSION   AF212604.1 GI:12003704
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SOURCE   Gibberella zeae
ORGANISM Gibberella zeae
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AUTHORS   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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TITLE     1 (bases 1 to 1336)
           O'Donnell, K., Kistler, H. C., Tacke, B. K. and Casper, H. H.
           Gene genealogies reveal global phylogeographic structure and
           reproductive isolation among lineages of Fusarium graminearum, the
           fungus causing wheat scab
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE   20345085
PUBMED    10869425
REFERENCE
AUTHORS   2 (bases 1 to 1336)
           O'Donnell, K.
DIRECT SUBMISSION
SUBMITTED (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
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RESULT 13

AF212582

LOCUS

DEFINITION

AF212582

VERSION

AF212582.1

GI:12003660

KEYWORDS

SOURCE

ORGANISM

Gibberella zeae

Gibberella zeae

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 1336)

O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.

Gene genealogies reveal global phylogeographic structure and

reproductive isolation among lineages of *Fusarium graminearum*, the

fungus causing wheat scab

Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)

20345085

10869425

2 (bases 1 to 1336)

O'Donnell, K.

Direct Submission

Submitted (08-DEC-1999) Microbial Properties Research,

NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA

Location/Qualifiers

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ACCESSION AF212583
VERSION AF212583.1 GI:12003662
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ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
TITLE Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
PUBMED 10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS O'Donnell, K.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Best local Similarity 95.4%; Pred. No. 0;
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LOCUS Gibberella zeae strain NRRL29010 trichothecene
DEFINITION 3-O-acetyltransferase, partial cds.

ACCESSION AF212584
VERSION AF212584.1 GI:12003664

KEYWORDS

SOURCE

ORGANISM

Gibberella zeae
Gibberella zeae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE

1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Take, B.K. and Casper, H.H.

Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab

Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)

20345085

10869425

REFERENCE 2 (bases 1 to 1336)

O'Donnell, K.

Direct Submission

Submitted (08-DEC-1999) Microbial Properties Research,

NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA

Location/Qualifiers

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Best Local Similarity 99.4%; Pred. No. 0;

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QY 781 ACTGACGATCTCTTTTCGCGCTTCATCTGAAATCGCCCTCTCGCGTGGCTTCGAAAGA 840
Db 783 ACTGACGATCTCTTTTCGCGCTTCATCTGAAATCGCCCTCTCGCGTGGCTTCGAAAGA 842
QY 841 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 900
Db 843 ATCGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 902
QY 901 GTCTCGAAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 960
Db 903 GTCTCGAAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 962
QY 961 GAAATCGCCAAACAGGTCACCTCGGCGCAACGACATACGCTTCGTTTTCAGAACTCGACCCC 1020
Db 963 GAAATCGCCAAACAGGTCACCTCGGCGCAACGACATACGCTTCGTTTTCAGAACTCGACCCC 1022
QY 1021 GCGAGATGGCGCAGGAAACAGAGGTCTCGGAGCTTCTGCAACAACACCCGACAAG 1080
Db 1023 GCGAGATGGCGCAGGAAACAGAGGTCTCGGAGCTTCTGCAACAACACCCGACAAG 1082
QY 1081 TCCAAAGTATCCCTGACGGCTGATCGGACCCCATCTACAGCGCTCATGCTGAGTCTTGG 1140
Db 1083 TCCAAAGTATCCCTGACGGCTGATCGGACCCCATCTACAGCGCTCATGCTGAGTCTTGG 1142
QY 1141 GCCAAGGTGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200
Db 1143 GCCAAGGTGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1202
QY 1201 AGACGCCCATCTTTGAGCGCTTGTGAGAGCTTGTACTTACTTATGCCAAGAGCCGCTGAT 1260

Mon Feb 9 08:28:53 2004

Db 1203 AGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCCAAGAAGCCTGAT 1262
QY 1261 GCGGAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACCCGATTTGAAGGCGGAT 1320
Db 1263 GCGGAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACCCGATTTGAAGGCGGAT 1322
QY 1321 AAGGAGTGGACCAA 1334
Db 1323 AAGGAGTGGACCAA 1336

Search completed: February 7, 2004, 20:53:19
Job time : 5224 secs

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OM protein - protein search, using sw model

Run on: February 7, 2004, 21:53:49 ; Search time 553 Seconds

(without alignments)
129.450 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAPKIQTLQLPGLLIY.....EDMDLKADKWKYQVQV 451

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	21 AAB03935	Trichothecene resi
2	2314	99.1	451	21 AAY51848	F. graminearum tri
3	1860.5	79.7	459	21 AAB03934	Trichothecene resi
4	962.5	41.2	474	21 AAB03936	Sequence encoding
5	170.5	7.3	424	21 AAG18711	Arabidopsis thalia
6	170.5	7.3	433	21 AAG18710	Arabidopsis thalia
7	170.5	7.3	436	24 ABUS8179	Wheat stress respo
8	170.5	7.3	450	21 AAG18709	Arabidopsis thalia
9	169.5	7.3	424	21 AAG48446	Arabidopsis thalia

10	169.5	7.3	433	21	AAG48445	Arabidopsis thalia
11	169.5	7.3	433	23	AB93749	Herbicidally activ
12	169.5	7.3	449	21	AAG48444	Arabidopsis thalia
13	168.5	7.2	446	24	ABUS8173	Corn stress respon
14	161	6.9	439	24	ABUS8177	Soybean stress res
15	156.5	6.7	442	23	AB93641	Herbicidally activ
16	154.5	6.6	431	21	AAB36457	Mango alcohol acyl
17	154	6.6	428	21	AAG24209	Arabidopsis thalia
18	154	6.6	440	21	AAG24208	Arabidopsis thalia
19	151.5	6.5	448	17	AAW04724	Aromatic acyl tran
20	151.5	6.5	459	23	AB92609	Herbicidally activ
21	149.5	6.4	450	23	AB92606	Herbicidally activ
22	149	6.4	648	23	AB92608	Herbicidally activ
23	146	6.3	443	23	AB92607	Herbicidally activ
24	143	6.1	441	21	AAG46685	Arabidopsis thalia
25	143	6.1	441	23	AB93668	Herbicidally activ
26	143	6.1	457	21	AAG46684	Arabidopsis thalia
27	143	6.1	475	23	AB93310	Herbicidally activ
28	142.5	6.1	426	21	AAG37720	Arabidopsis thalia
29	142.5	6.1	426	21	AAG37735	Arabidopsis thalia
30	142.5	6.1	426	23	AB93930	Herbicidally activ
31	142.5	6.1	438	21	AAG37734	Arabidopsis thalia
32	142.5	6.1	442	21	AAG37719	Arabidopsis thalia
33	142	6.1	448	22	AAE00254	Taxus cuspidata fu
34	141.5	6.1	436	23	AB91119	Herbicidally activ
35	138.5	5.9	327	21	AAG46686	Arabidopsis thalia
36	134.5	5.8	448	21	AAG21060	Arabidopsis thalia
37	134.5	5.8	448	23	AB93980	Herbicidally activ
38	134.5	5.8	455	21	AAG21059	Arabidopsis thalia
39	134	5.7	448	15	AA47475	Polypeptide encode
40	134	5.7	448	15	AA46929	Tobacco Ant32 geno
41	132.5	5.7	313	21	AAG25750	Arabidopsis thalia
42	132.5	5.7	479	21	AAG45712	Arabidopsis thalia
43	132.5	5.7	484	21	AAG45711	Arabidopsis thalia
44	132.5	5.7	484	23	AB93588	Herbicidally activ
45	132	5.7	439	22	AAE00240	Taxus cuspidata fu

ALIGNMENTS

RESULT 1
AAB03935
ID AAB03935 standard; Protein; 451 AA.
XX AAB03935;
AC
XX
DT 26-FEB-2001 (first entry)
DE Trichothecene resistance polypeptide.
XX
KW Trichothecene resistance; resistant; crop protection; mycotoxin;
KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium.
XX
OS Fusarium graminearum.
XX
FN WO2000060061-A2.
XX
PD 12-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-EP02769.
XX
PR 31-MAR-1999; 99US-0282995.
PR 11-FEB-2000; 2000US-0502852.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Hohn TW, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
DR N-PSDB; AAA54209.
DR

XX Plant cell for preventing mycotoxin contamination of wheat, maize,
 PT barley or rice plant, comprises heterologous polynucleotide encoding
 PT gene product expressed in cell, having trichothecene resistance
 PT activity
 XX
 PS Claim 15; Page 49-50; 62pp; English.
 XX
 CC A heterologous gene encoding a gene product which confers
 CC trichothecene resistance can be used to transform plant cells to
 CC make them resistant to fungal infection. The transformation method is
 CC useful for preventing mycotoxin contamination of a plant,
 CC particularly a crop plant such as wheat, maize, barley or rice, and
 CC for reducing and/or preventing the growth of a fungus of the genus
 CC Fusarium that produces a trichothecene, preferably comprising a C-3
 CC hydroxyl group, by growing transformed crop plants in an area which
 CC is moderate to severe fungal infestation.
 XX
 SQ Sequence 451 AA;

Query Match 100.0%; Score 2334; DB 21; Length 451;
 Best Local Similarity 100.0%; Pred. No. 5.4e-211;
 Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFKIQDITLQGLPGLLSIYQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
 DB 1 MAFKIQDITLQGLPGLLSIYQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
 QY 61 KAEGISEGNTGTSFIVPEFVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPRK 120
 DB 61 KAEGISEGNTGTSFIVPEFVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPRK 120
 QY 121 TLPGPCTGDDPKPVLILQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
 DB 121 TLPGPCTGDDPKPVLILQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
 QY 181 TEEMTAMNLDRTKTIIVPELYNTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
 DB 181 TEEMTAMNLDRTKTIIVPELYNTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
 QY 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
 DB 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
 QY 301 VSNYPGLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
 DB 301 VSNYPGLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
 QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420
 DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420
 QY 421 GEFCAALSRLRDEMDRLKADKEWTKYAYVG 451
 DB 421 GEFCAALSRLRDEMDRLKADKEWTKYAYVG 451

RESULT 2
 AAY51848
 ID AAY51848 standard; Protein; 451 AA.
 XX
 AC AAY51848;
 XX
 DT 09-JUN-2000 (first entry)
 XX
 DE F. graminearum trichothecene 3-O-acetyltransferase protein.
 XX
 KW Trichothecene 3-O-acetyltransferase; selective marker.
 XX
 OS Fusarium graminearum.
 XX
 FN JP2000032985-A.

PD 02-FEB-2000.
 XX
 PF 15-JUL-1998; 98JP-0200280.
 XX
 PR 15-JUL-1998; 98JP-0200280.
 XX
 PA (RIKA) RIKAGAKU KENKYUSHO.
 PA (YAMA/) YAMAGUCHI I.
 XX
 DR WPI; 2000-274037/24.
 DR N-PSDB; AAY51848.
 XX
 PT Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
 XX gene manipulations in eukaryotic host cells -
 PS Claim 1a; Page 18-19; 25pp; Japanese.
 XX
 CC This invention describes a novel protein with trichothecin
 CC 3-O-acetyltransferase activity. The gene is used as a selective marker
 CC in a gene manipulation using eukaryote as the host cell. This sequence
 CC represents the trichothecin 3-O-acetyltransferase isolated from
 CC Fusarium graminearum.
 CC
 XX Sequence 451 AA;

Query Match 99.1%; Score 2314; DB 21; Length 451;
 Best Local Similarity 99.1%; Pred. No. 4.2e-209;
 Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAFKIQDITLQGLPGLLSIYQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
 DB 1 MAFKIQDITLQGLPGLLSIYQISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
 QY 61 KAEGISEGNTGTSFIVPEFVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPRK 120
 DB 61 KAEGISEGNTGTSFIVPEFVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPRK 120
 QY 121 TLPGPCTGDDPKPVLILQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
 DB 121 TLPGPCTGDDPKPVLILQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
 QY 181 TEEMTAMNLDRTKTIIVPELYNTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
 DB 181 TEEMTAMNLDRTKTIIVPELYNTIGPEVDHQIVKADVAGGDAVLTVPVSASWAFTFSPKA 240
 QY 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
 DB 241 MSELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAWG 300
 QY 301 VSNYPGLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
 DB 301 VSNYPGLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
 QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420
 DB 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEPVESLMYFMPKKPD 420
 QY 421 GEFCAALSRLRDEMDRLKADKEWTKYAYVG 451
 DB 421 GEFCAALSRLRDEMDRLKADKEWTKYAYVG 451

RESULT 3
 AAB03934
 ID AAB03934 standard; Protein; 459 AA.
 XX
 AC AAB03934;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Trichothecene resistance polypeptide.
 XX
 KW Trichothecene resistance; resistant; crop protection; mycotoxin;

KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium.
XX Fusarium sporotrichioides.
OS WO200060061-A2.
XX 12-OCT-2000.
XX 29-MAR-2000; 2000WO-EP02769.
XX 31-MAR-1999; 99US-0282995.
XX 11-FEB-2000; 2000US-0502852.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
XX N-PSDB; AAA54206.
XX Plant cell for preventing mycotoxin contamination of wheat, maize,
XX barley or rice plant, comprises heterologous polynucleotide encoding
PT gene product expressed in cell, having trichothecene resistance
PT activity
XX Claim 15; Page 46-48; 62pp; English.
XX A heterologous gene encoding a gene product which confers
XX trichothecene resistance can be used to transform plant cells to
XX make them resistant to fungal infection. The transformation method is
XX useful for preventing mycotoxin contamination of a plant,
XX particularly a crop plant such as wheat, maize, barley or rice, and
XX for reducing and/or preventing the growth of a fungus of the genus
XX Fusarium that produces a trichothecene, preferably comprising a C-3
XX hydroxyl group, by growing transformed crop plants in an area which
XX is moderate to severe fungal infestation.
XX Sequence 459 AA;
Query Match 79.7%; Score 1860.5; DB 21; Length 459;
Best Local Similarity 77.6%; Pred. No. 2.4e-166;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKIQDITGQLPGLLSYITQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK 61
DB 11 SFDIELDIIGQOPPELLSYITQISLLYPVSDSSQYPTIVSTFEQGLKRLSQTFFPWVAGQVK 70
QY 62 AEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFDENIAPRKT 121
DB 71 TEGISEGNTGTSKIIPYEETPLRVVKDLRDDPSAPTIEGMRKAGYPMAFDENIAPRKT 130
QY 122 LPIGFGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPPT 181
DB 131 LAIGFNGPNDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNEFT 190
QY 182 EEMTAMNLDKRTIYPIYENYITIGPEVDHQIADVAGGDAVLTVPVSASWAFPTFSPKAM 241
DB 191 EEEISAMNLDKRTVPLENYKVGPELDHQIADVAGGDAVLTVPVSASWAFPTFSPKAL 249
QY 242 SELKDAATKTLDASTKFSVSTDDALSAFTWKSASRVLRIDGSAFTFCRAVDARPAWGV 301
DB 250 SELKDAATKTLDASTKFSVSTDDALSAFTWQSTSRVRLARLDASTTEFCRAVDMRGPMGV 309
QY 302 SNNYEGLLQNNYHNTSTIGETANESIGATSELRSELDPSANRORTGLATYLNHNDPS 361
DB 310 SSTYEGLLQNNYHNTSTIGETANESIGATSELRSELDPSANRORTGLATYLNHNDPS 369
QY 362 NVSLTADAPDSTVMSLSSWAKVGLMDYDFGLGKGPETVRRPIFPFVBSLMYFMPKPKDG 421
DB 370 SVSLTADANPSSIMLSWAKVGCWEYDFGLGKGPESVRRPFRPFESLMYFMPKPKPDG 429

QY 422 EFCALSLRDEMDRLKADKEWTKYQAVVG 451
DB 430 EFTASISLRDEMDRLKADKEWTKYQAVVG 459
RESULT 4
AAB03936
ID AAB03936 standard; Protein; 474 AA.
XX AAB03936;
XX 26-FEB-2001 (first entry)
XX Sequence encoding trichothecene resistance polypeptide.
XX Trichothecene resistance; resistant; crop protection; mycotoxin;
KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium.
XX Saccharomyces cerevisiae.
OS WO200060061-A2.
XX 12-OCT-2000.
XX 29-MAR-2000; 2000WO-EP02769.
XX 31-MAR-1999; 99US-0282995.
XX 11-FEB-2000; 2000US-0502852.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
XX N-PSDB; AAA54210.
XX Plant cell for preventing mycotoxin contamination of wheat, maize,
XX barley or rice plant, comprises heterologous polynucleotide encoding
PT gene product expressed in cell, having trichothecene resistance
PT activity
XX Claim 15; Page 51-52; 62pp; English.
XX A heterologous gene encoding a gene product which confers
XX trichothecene resistance can be used to transform plant cells to
XX make them resistant to fungal infection. The transformation method is
XX useful for preventing mycotoxin contamination of a plant,
XX particularly a crop plant such as wheat, maize, barley or rice, and
XX for reducing and/or preventing the growth of a fungus of the genus
XX Fusarium that produces a trichothecene, preferably comprising a C-3
XX hydroxyl group, by growing transformed crop plants in an area which
XX is moderate to severe fungal infestation.
XX Sequence 474 AA;
Query Match 41.2%; Score 962.5; DB 21; Length 474;
Best Local Similarity 44.4%; Pred. No. 1.2e-81;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;
QY 6 QLDITGQLPGLLSYITQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKARGI 65
DB 22 QLDITGQLPGLLSYITQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKARGI 81
QY 66 SEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFDENIAPRKT-LPI 124
DB 82 DEGNTGTVRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFPYMLDEKTPACMTINPP 140
QY 125 GPGTG-PDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPPTFEE 183
DB 141 GNTIGMAAKSPFVAVQANFISGGVLTIVQHNIMDITGQESINLNLKSKCHQKPFSD 200

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 05-MAY-1999; 99US-0132485.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
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PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 7.3%; Score 170.5; DB 21; Length 433;
Best Local Similarity 23.4%; Pred. No. 4.8e-07;
Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

QY 36 PTVSTF--EQLGR-FGEA-VPW--VAGOVKAEG-----ISEGNTGTSFIVPFEDVERV 84
DB 44 PTGASFFDPQVWKALSKALVPFFPMAGRLKRDGRIEDCNAGVLFFV--ADTFSV 101

QY 85 VVKLRDP--PSAPTIEGRKAGYPMAMPDENIIAPRKTLP-IGPTGPDPPKPVILLQL 141
DB 102 I-----DDFGDPATL-----NL---RLIPEVDHSTGIHS-FPLLVLQV 137

QY 142 NFIK-GGLITVNGHGMDVQDAVIRLLSKACNRNPFTEEMTAMMLDKRTIVPYLE 200
DB 138 TFFKCGGASLGVGMQHAADGSLHFNITWSDMAR-----GLD----- 176

QY 201 NVTIGPEVDHQTVKA-----DVAGGDAVLTPVSASWAFFTSPKAM 241
DB 177 -LTPPFIDRIILLRARDPPQAFHVEYQAPSMKIPILDPKSGPENTTVSIFKLRDQL 235

QY 242 SELKDAATKTLDASTKFTSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDA----RP 297
DB 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSLRP 291

QY 298 AMGVSNYPGLLONTYINSTI-----GEIANESLGATASRLRSLDPAS 342
DB 292 QLP-----PGYFGNVIFATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD--- 343

QY 343 MKQRTGRGLATYLNHPDKNSVSLTADAPTSVMSLWAKVGLWYDFGLGKGPETVRR 402
DB 344 -----YLEMOPDLSALVRGHANTYKCPNGLGTSWRLPIYDADFGWG-----R 385

QY 403 PIFE-----PVESLMYFMFKKP-DGEFCAALSRLDEDM 434
DB 386 PIFMGPGGIPYEGLSFVLPSPTNDGSLVAIALQSEHM 423

RESULT 7
ID ABU58179 standard; Protein; 436 AA.
AC ABU58179;
XX
DT 14-APR-2003 (first entry)
DE Wheat stress response protein #7.
XX
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KW Plant; EST; expressed sequence tag; stress response; drought;
KW heat; radiation; pathogen attack; grain flavour; disease resistance;
KW peptide-methionine sulfoxide reductase; DNA repair; enzyme;
KW intracellular protein transport.
XX
OS Triticum aestivum.
PN US2002152497-A1.
XX 17-OCT-2002.
XX 19-FEB-2002; 2002US-0078929.
XX 07-MAY-1999; 99US-133038P.
XX 07-MAY-1999; 99US-133042P.
XX 11-MAY-1999; 99US-133427P.
XX 11-MAY-1999; 99US-133428P.
XX 11-MAY-1999; 99US-133436P.
XX 11-MAY-1999; 99US-133437P.
XX 11-MAY-1999; 99US-133438P.
XX 04-JUN-1999; 99US-137667P.
XX 05-MAY-2000; 2000US-0566394.
XX (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAXA/) SAKAI H.
PA (WENG/) WENG Z.
XX
PI Falco SC, Famodu OO, Meyers BC, Miao G, Odell JT, Rafalski JA,
PI Thorpe CJ, Sakai H, Weng Z;
XX
DR WPI: 2003-198391/19.
DR N-PSDB; AEX78350.
XX
PT New peptide-methionine sulfoxide reductase and nucleic acids, useful in
PT improving plant response to stress, engineering plants with increased
PT disease and stress resistance, or and improving/protecting grain flavor
PT
XX Claim 1; Fig 4; 205pp; English.
XX
CC The invention relates to isolated nucleic acids encoding plant stress
CC response proteins (including peptide-methionine sulfoxide
CC reductases) appearing as ABU58148-ABU58246 (or a protein 80% identical
CC to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum.
CC Also included are expression cassettes, transformed host cells,
CC transgenic plants/seeds, modulating the level of peptide-methionine
CC sulfoxide reductase in a plant and a computer system/data
CC processing system for identifying, analysing, or modelling a genetic
CC sequence. The plant nucleic acid is useful in developing strategies to
CC improve plant response to stress (e.g. drought, heat, radiation or
CC pathogen attack), engineering plants with increased disease and stress
CC resistance, manipulating DNA repair and recombination efficiency,
CC manipulating intracellular protein transport, and improving/protecting
CC grain flavour. The nucleic acids may also be used as probes or
CC amplification primers in the detection, quantitation or isolation of gene
CC transcripts, for recombinant expression of encoded polypeptides, as
CC immunogens in preparing or screening antibodies, and in sense or
CC antisense suppression of one or more genes in a host cell, tissue or
CC plant. The proteins may be used as immunogens or antigens to obtain
CC antibodies specifically immunoreactive with the protein, and in assays
CC for enzyme agonists or antagonists. The present sequence is a plant
CC stress response protein (or fragment).
XX
SQ Sequence 436 AA;
Query Match 7.3%; Score 170.5; DB 24; Length 436;
Best Local Similarity 20.4%; Pred. No. 4.9e-07;
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Matches 84; Conservative 61; Mismatches 158; Indels 109; Gaps 15;	
QY 56 VACQVKAEGISEGN-----TGTSFIVPEDEVRVVKDLRDDPSATTIEGMRKAGYFMA 109	PR 06-MAY-1999; 99US-0132487.
Db 78 LAGELGREG--EGGRLOIDCNGEGALFVLARAPDVAGEDLFGSGYEPSPE-IRRMFVYFPA 134	PR 07-MAY-1999; 99US-0132863.
QY 110 MFDENIAPKTLPIGPGTGPDPKPVILLQLNFIK--GGILITVNGOGGAMDMVGGQDAVI 168	PR 11-MAY-1999; 99US-0134256.
Db 135 -----PSG-----DPCHNAMEQVTFKCGGVVLGTGIIHVTMDGNGAFHI 176	PR 14-MAY-1999; 99US-0134218.
QY 169 RL-----LSKACRNDPTEEMTAMNLDRTKIYVYLENYTIGPEVHQIVKADVAG 219	PR 14-MAY-1999; 99US-0134219.
Db 177 QTWTGLARGLSLSEACSPFHDRTLLRASPFR-----PEFEHPVYSPAYLN 224	PR 14-MAY-1999; 99US-0134221.
QY 220 GDAVLPVSASWAFFTFSPKAMSELKDAATKTLDASTKFFVSTDDALSATFK----- 271	PR 18-MAY-1999; 99US-0134370.
Db 225 G----APRPVTRVYSVQKLLADIKSRCAPG-----VSTYGAVTAHLWRCMCVARGL 273	PR 18-MAY-1999; 99US-0134378.
QY 272 ---SASRVRL-----ERIDGSAPTEFCRAVDARPAMGVSNNNYPGILLQNMVTHNSTIGEIA 323	PR 19-MAY-1999; 99US-0134421.
Db 274 APGSDTFLRPANIRHRLRPQLPRQFFGNALVRDLTVK-----VGDVL 317	PR 20-MAY-1999; 99US-0135124.
QY 324 NESIGATASRLSELDPASMRQRTGLATYLNHNPDKSNVSLTADADPSTVMLSSWAKV 383	PR 21-MAY-1999; 99US-0135353.
Db 318 SQPLGYVADTIRKAVDHVD--DAYTRSVIDYLEVESEKGSQAARGQLMPESDLWVWSLGM 376	PR 24-MAY-1999; 99US-0135629.
QY 384 GLWDYDFGLGKPEYTRRPIFEPVESLMYFMPKPKPDGEFCAALSLEDEMD 435	PR 25-MAY-1999; 99US-0136021.
Db 377 PMYDADFQWAPR-----FVAPAQMFSGTAYVTQCADRD 412	PR 27-MAY-1999; 99US-0136392.
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XX 17-OCT-2000 (first entry)	PR 03-JUN-1999; 99US-0137528.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20227.	PR 04-JUN-1999; 99US-0137528.
KW Protein identification; signal transduction pathway; metabolic pathway;	PR 07-JUN-1999; 99US-0137724.
KW hybridisation assay; genetic mapping; gene expression control; promoter;	PR 08-JUN-1999; 99US-0138094.
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OS Arabidopsis thaliana.	PR 10-JUN-1999; 99US-0138847.
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XX 25-FEB-1999; 99US-0121825.	PR 17-JUN-1999; 99US-0139492.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
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PR 29-OCT-1999; 99US-0162142.

Query Match 7.3%; Score 170.5; DB 21; Length 450;
Best Local Similarity 23.4%; Pred. No. 5.1e-07;
Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

QY 36 PTIVSTF--EQGLKR-FSEA-VPW--VAGQVKRG-----ISEGNTGTSFIVPVEDVPRV 84
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QY 85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIAPKTLF-IGBGTGPDGPKPVILLQL 141
Db 119 I-----DDFGDPAPTL-----NL-----ROLIPEVDHSTGIHS-FPLLVLQV 154
QY 142 NFIK-GGLIIVNGQHGAMDVGQDAVIRLLSKACRNDPFTTEEBMTAMNLRKTIIVPYLE 200
Db 155 TFFKCGGASLGVGMQHHADGFGSLHFINWSDMAR-----GLD----- 193
QY 201 NYTIGPEVDHIOVKA-----DVAGGDAVLTPVSASNAFFTFSPKAM 241
Db 194 -LTIPPFIDRTLRRADPPQPAFHVEYQAPAPSMKIPLDPSKGPENTVTSIFKLTRDQL 252
QY 242 SELKDAATKTLDASTKFKVSTDDALS AFTWKSASRVLERIDGSAFTFCRAVDA----RP 297
Db 253 VALK--AKSKEDGNTVSYSYEMLAGHVWRSVGKAR--GLPNDQETKLIYATDGRSLRP 308
QY 298 AMGVSNYPGLQNNYHNSIT-----GEIANESIGATASRLRSELDPAS 342
Db 309 QLP-----PGYFGNVITATPLAVAGDLLSKPTWVAGQIHDFLVRMDDNVIRSALD--- 360
QY 343 MRQTRGLATYLNHNPNKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRR 402
Db 361 -----YLEMQPDL SALVRGAHTYKCNLGTISVRLPIYDADFVGW-----R 402
QY 403 PIFB-----PVESLMYFMEKXP-DGEFCAALSRLDEDM 434
Db 403 PIFMGPGIPIYEGLSFVLPSPTNDGSLVALQSEHM 440

RESULT 9
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AC AAG48446;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 61177.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX AC ABB93641;
XX DT 31-MAY-2002 (first entry)
XX DE Herbicidally active polypeptide SEQ ID NO 2852.
XX KW Herbicidal; plant; agriculture; herbicide.
XX OS Arabidopsis thaliana.
XX PN WO200210210-A2.
XX PD 07-FEB-2002.
XX PF 28-AUG-2001; 2001WO-EP09892.
XX PR 28-AUG-2001; 2001WO-EP09892.
XX PA (FARB ) BAYER AG.
XX PI Tietjen K, Weidler M;
XX DR WPI; 2002-269010/31.
XX PT Identifying plant target proteins for herbicidally active compounds,
XX FT comprising aligning and comparing nucleic acid or amino acid sequences
XX FT from plant with nucleic acid or amino acid sequences from non-plant
XX FT organisms -
XX PS Claim 5; SEQ ID NO 2852; 261pp + Sequence Listing; English.
XX CC The invention relates to identifying target proteins
XX CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX CC aligning and comparing nucleic acid or amino acid sequences from plant
XX CC with nucleic acid or amino acid sequences from non-plant organisms using
XX CC suitable search parameters, where plant sequences having an E-value
XX CC greater by a factor of 3 than the E-value of most similar non-plant
XX CC sequences are selected. The polypeptides or nucleic acids encoding them
XX CC are useful for identifying modulators. The identified modulators are
XX CC useful as herbicides.
XX SQ Sequence 442 AA;

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ALIGNMENTS

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; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dilli-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-09-538-414-6

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Qy	181	TEEMTAMNLDRTKI	VPYLENY	TIGPEVDHQIWKADVAGGDAVLTVPVSASWAFETSPKA	240		
Db	181	TEEMTAMNLDRTKI	VPYLENY	TIGPEVDHQIWKADVAGGDAVLTVPVSASWAFETSPKA	240		
Qy	241	MSELKDAATKTLDA	STKFKVST	DDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG	300		
Db	241	MSELKDAATKTLDA	STKFKVST	DDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPMG	300		
Qy	301	VSNNYFGLLQNTY	HNSTTGE	ITANESIGATASRLSELDPASMRQTRGLATYIHNNPDK	360		
Db	301	VSNNYFGLLQNTY	HNSTTGE	ITANESIGATASRLSELDPASMRQTRGLATYIHNNPDK	360		

Db 301 VSNVYGLLQNNYTHNSTIGIEANESLGATASRLSELDPASMRQRTGLATYLNHPDK 360

QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLWYFMPKPD 420

Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLWYFMPKPD 420

QY 421 GEFCAALSURDEMDRLKADKWKYAOYVG 451

Db 421 GEFCAALSURDEMDRLKADKWKYAOYVG 451

RESULT 2

US-09-538-414-2

; Sequence 2, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequencelist

; CURRENT APPLICATION NUMBER: US/09/538,414

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 2

; LENGTH: 459

; TYPE: PRT

; ORGANISM: Fusarium sporotrichioides

US-09-538-414-2

Query Match 79.7%; Score 1860.5; DB 4; Length 459;

Best Local Similarity 77.6%; Pred. No. 1e-184;

Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;

QY 2 AFKIDTLGQLGLLSIYQISLLYPVSDSSQVPTIVSTFEOGLKRFSEAVPWVAGQVK 61

Db 11 SFDIELDIICQPPLLSIYQISLLYPVSDSSQVPTIVSTFEOGLKRLSQTFFPWVAGQVK 70

QY 62 AEGISGNTGTSFIVPEFPRVVKDLRDDPSAPTTGMRKAGYPMAMFENIIAPRKT 121

Db 71 TEGISEGNTGTSKLIIPYEETPRLVVKDLRDDSSAPTTGMRKAGYPMAMFENIIAPRKT 130

QY 122 LPICPGTGPDDPKPVILLQNLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNDPFT 181

Db 131 LAIGPGNGPNDPKFVLLQNLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNSFT 190

QY 182 EEMTAMNLDRTKIVPVLENYTIGPEVDHQLVKADVAGDAVLTVPVSAWAFPTFSKAM 241

Db 191 EEBISAMNLDRTKIVPVLENYTIGPEVDHQLVKADVAGDAVLTVPVSAWAFPTFSKAL 249

QY 242 SELKDAATKLDASTKFVSTDDALSATFWKSASRVRLERIDGSAPTEFCRAVDARPA 301

Db 250 SELKDAATKLDASTKFVSTDDALSATFWKSASRVRLERIDGSAPTEFCRAVDARPA 309

QY 302 SNVYGLLQNNYTHNSTIGIEANESLGATASRLSELDPASMRQRTGLATYLNHPDKS 361

Db 310 SSVYGLLQNNYTHNSTIGIEANESLGATASRLSELDPASMRQRTGLATYLNHPDKS 369

QY 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLWYFMPKPDG 421

Db 370 SVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLWYFMPKPDG 429

QY 422 EFCALSURDEMDRLKADKWKYAOYVG 451

Db 430 EFTASISURDEMDRLKADKWKYAOYVG 459

RESULT 3

US-09-538-414-8

; Sequence 8, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequencelist

; CURRENT APPLICATION NUMBER: US/09/538,414

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 8

; LENGTH: 474

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-09-538-414-8

Query Match 41.2%; Score 962.5; DB 4; Length 474;

Best Local Similarity 44.4%; Pred. No. 2.9e-91;

Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;

QY 6 QLDITGLGQLGLLSIYQISLLYPVSDSSQVPTIVSTFEOGLKRFSEAVPWVAGQVKARGI 65

Db 22 QLDITGLGQLGLLSIYQISLLYPVSDSSQVPTIVSTFEOGLKRFSEAVPWVAGQVKARGI 81

QY 66 SEGNTGTSFIVPEFPRVVKDLRDDPSAPTTGMRKAGYPMAMFENIIAPRKT-PI 124

Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSLEKADFPIYMLDEKTFAPCMTINPP 140

QY 125 GPOTG-PDDPKPVILLQNLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNDPETER 183

Db 141 GNTIGMAAKSGPVFAVQANFISGGLVLTIVGQHNIMDITQGESIINLNLKSKCHQKPFSD 200

QY 184 EMTAMNLDRTKIVPVLENYTIGPEVD--HOIVKA--DVAGDAVLTVPV--ASWAFPTFS 238

Db 201 ELLIGNIDKSKSLPDE-TWEPDTLVHVEIVTSRNTSGEKEQSCSSNSTWAYVFSA 259

QY 239 KAMSELKDAATKLDASTKFVSTDDALSATFWKSASRVRLERIDGSAPTEFCRAVDARPA 298

Db 260 ISLQNLRIILAMQCTSGTKFVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVVRKR 319

QY 299 MGVSNNYVGLLQNNYTHNSTIGIEANESLGATASRLSELDP--SMRQRTGLATYLN 356

Db 320 LGLPETYPGLLVNMTNTGSLKSLDHKSLGLVLAQIRKLDPKVDFDIAYNTCALATLLSR 379

QY 357 NPKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRPIPEPVESLWYFMP 416

Db 380 CPDKTKVSIQPDITLSCGIVSWWAKVSLVDVDFNLGLGKPKSVRRPRFISLESILYFMP 439

QY 417 KPDGGEFCAALSURDEMDRLKADKWKYAOYVG 451

Db 440 RSSRGEVNVVALCLRDKDWECINADKENTVATNATHIG 474

RESULT 4

US-09-457-046B-56

; Sequence 56, Application US/09457046B

; Patent No. 6287835

; GENERAL INFORMATION:

; APPLICANT: Crocean, Rodney et al.

; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

; FILE REFERENCE: 53679

; CURRENT APPLICATION NUMBER: US/09/457,046B

; CURRENT FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 56

Db 180 LGNEPH-----DRKFLRAGEPPYATFHEHQNP-----PPLLGGSS- 220
QY 232 APFTFSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIKWSASRVL 278
Db 221 -----EEEKNETKSGMLKLTQHVEMLRKKANQGRSYTRYEVVTAHWACKARG 275
QY 279 ERIDGSAPTFCFCAVDARPA--GVSNNYPGLLQNTYHNSITIGETANESLGATASRLS 336
Db 276 HKFE--OPTNLCTICVNIRNIMQPLPKSYFGNAIVDIANGVSGDITSRPLEVAVRVR- 332
QY 337 ELDPSMRQRTGLAT-----YLHNNPKSNVSLTAD-----ADPSTSVMLSSW 380
Db 333 -----AAIKWTSYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPLGVI--SW 383
QY 381 AKVGLWDYDFGLGKPEVRRRIFEPVESLMTFMP-KKPDGFCAALSRLDEDMRLK 438
Db 384 ISPLLLGLDFGWG---KEIHMSPTHEYDGDGVILPCKEGDGLTVAIILQAVHVDFAK 439

RESULT 7

US-08-207-904-17
; Sequence 17, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; APPLICANT: Crossland, Lytle D.
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,904
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-904-17

Query Match 5.7%; Score 134; DB 1; Length 448;

Best Local Similarity 21.7%; Pred. No. 4e-05;

Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

QY 21 TQISLLY-----PVSDSSQYPTIVSTEQGLK-----PSEAVPWWAGQVKAEG 64
Db 34 THVPTIYRFFCHDCLPSTDN-----IKTURTSLSKALVHFYPLSGRLWIAG-----S 83
QY 65 ISEGNIGTSFTVPPEDVRVVKDLRDDPSAPTIEGMRKAGYPMFMDENIAPR--KTL 122

Db 84 RLELDCNAGSIVLMRAETEAKLDDLDGDFSPS-----DLNSLFPVDYTI 128
QY 123 PTGPGTGPDPKPVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179
Db 129 PI-----DELPLLFVQLTKFCQGGIALSFAISHAVD--GOSALYFLTEWASLARGEP 179
QY 180 FTEETEAMNLDKTI-----VPLENYITIGPEVDHQIVKADVAGGDAVITPVSAW 231
Db 180 LGNEPH-----DRKFLRAGEPPYATFHEHQNP-----PPLLGGSS- 220
QY 232 APFTFSPKAMSELKDAATKTLDASTKFV-----STDDALSAPIKWSASRVL 278
Db 221 -----EEEKNETKSGMLKLTQHVEMLRKKANQGRSYTRYEVVTAHWACKARG 275
QY 279 ERIDGSAPTFCFCAVDARPA--GVSNNYPGLLQNTYHNSITIGETANESLGATASRLS 336
Db 276 HKFE--OPTNLCTICVNIRNIMQPLPKSYFGNAIVDIANGVSGDITSRPLEVAVRVR- 332
QY 337 ELDPSMRQRTGLAT-----YLHNNPKSNVSLTAD-----ADPSTSVMLSSW 380
Db 333 -----AAIKWTSYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPLGVI--SW 383
QY 381 AKVGLWDYDFGLGKPEVRRRIFEPVESLMTFMP-KKPDGFCAALSRLDEDMRLK 438
Db 384 ISPLLLGLDFGWG---KEIHMSPTHEYDGDGVILPCKEGDGLTVAIILQAVHVDFAK 439

RESULT 8

US-09-457-046B-28
; Sequence 28, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 28
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-28

Query Match 5.7%; Score 132; DB 3; Length 439;

Best Local Similarity 20.0%; Pred. No. 6.3e-05;

Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21;

QY 5 IQDLTLGQLPGLLSIYTOISLLYPVSDSSQYPTIVST-----PEQGLKRFSEAVPWWAGQ 59
Db 27 LQLSSIDNLPVGRGSIENALLIYNAPS---PTMISADPAKPIREALAKILVYPPFAGR 83
QY 60 VK-----ARGISEGNTGTSFTIVPPEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMF 111
Db 84 LRETENGDLVEBCTGE---GAMFLEAMADNELSVLGDG---DDSNPSFQOL-----LF 130
QY 112 DENIIAPRKTLPIGPGTGPDPKPVILLQLNFIKGLIILTVNGQHGAMDMVGQDAVIRLL 171
Db 131 -----SLPL--DTNFKDLSLLVVQVTRFTCGGFVVGVSFFHGHVCDGRGAQFLLKGL 179
QY 172 SKACRN-----DPFTEEMTAMNLDKTI VPLENYITIGPEVDHQIVKADVAGGDAVLT 225
Db 180 AEMARGEVKLSLEPIWNRELVKLD-DPKYLQFFHFEFLRAPSIVEKIVQ----- 227
QY 226 PVSASNAFFTFSPKAMSELKDAATKTLDASTKYFVSTDDALSAPIKWSASRVLRIIDGSA 285
Db 228 -----TVFIIDFTETINVIKQS-----VMECKEFCFSFEVASAMTW--IARTRAFQIPESE 276
QY 286 PTEFCRAVDARPAWGVSNNYPGLLQNTYHNS--TIGETANESLGATASRLS---ELD 339
Db 277 YVKILFGDMR-----NSFNPLPSGYIGNSIGTACAVDINVQDLLSGSLLRIMLIKKS 330

```
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 69
; LENGTH: 451
; TYPE: PRN
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-69

Query Match      5.6%; Score 130.5; DB 3; Length 451;
Best Local Similarity 21.7%; Pred. No. 9.4e-05;
Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;

QY 8 DTLGQLPGLLSIYTOISLLYPVSDSQVPTIVSTFEQGLKRFSEAVPWVAGQVX----- 61
Db 29 DQVGTITHTIPTL-----FYDKPSESFGQNVVEILKTSLSRVLVHFYPMAGRLWLPGR 83
QY 62 -----AEGI-----SENGTGTSTFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPM 109
Db 84 FELNCNAGVEFIEAESEK-----LSDFKDFSTPEFENL----- 119
QY 110 MFDENIIAPRTLPITPGTGPDPKPVILLQLNFI--GGILITVNGQHGAMDMVGQDAVI 168
Db 120 MPQVYNKPIETIPL-----FLAQVTFKCGGISLVNVSVAIVD--GQSA-L 164
QY 169 RLLS--KACNDPTEEMTAMNLDRTI--VPYLENTYIGPEVDHQ----- 211
Db 165 HLISEWGLRGLGEPL-----TVPELDRKILWAGER-LPPFVSPPKFDHKEFDQPPFLIGE 219
QY 212 --IVKADVAGDAVLTVPVSAWAFTEFSPKAMSELKDA--TKILDASTKFSVTDALSA 267
Db 220 TDNVEERKKKTIIVMLPLSTS-----QLQKLRSKANGSKHSDPAKGP-TRYETVTG 269
QY 268 FPKASRVRLEIDGSAPEFCRAVDARPAM--GVSNYPGLLQNMVYHNSITIGETANE 325
Db 270 HWRCACKARGH--SPQPTALGICIDTRSMEEPPLRGYFGNATLDVVAASTSGELISN 327
QY 326 SLGATASRLSELDPASMRQTRGLATYLVHNNPD--KSNVSLTA-----DADPSTSYM 376
Db 328 ELGFAASLSIAKIKVNTNEYVMIGI-EYLKXQDKLKKFQDLHALGSTEGPPYGNPLGVV 386
QY 377 LSSWAKVGLWDYDGLGKGPETVRPIFEVESLMYFMP-KKPDGFECAALSDEDM 435
Db 387 --SMITPMYGLDFGWG---KEFTYGTGTHDFDGSILPLQDNEDSGSVILATCLQVHME 441
QY 436 RLK 438
Db 442 AFK 444

RESULT 10
US-09-457-046B-60
; Sequence 60, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 68
; LENGTH: 439
; TYPE: PRN
; ORGANISM: Catharanthus roseus
US-09-457-046B-60

Query Match      5.4%; Score 126.5; DB 3; Length 435;
Best Local Similarity 20.2%; Pred. No. 0.00023;
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

QY 4 KIQLDTLG-QLPGLLSIYTOISLLYP-VSDSQVPTIVSTFEQGLK-----RFSEAVPWV 56
Db 23 RLQLSILDLYCPG---IYVSTIFFYDLITSESE-----VFSENKLKLSLSETLSRFYP-L 72
QY 57 AGOVKAEGISGNTGTSTFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMFENII 116
Db 73 AGRIEGLISCNDEGAVTEARTD---LILLPDFLRNLNLTDSLSGF----- 114
QY 117 APRKTLF-IGFGTGDPDPKPVILLQLNFI--KGGILITVNGQHGAMDMVGQDAVIRILSK 173
Db 115 -----LPTLAAGESP-AAWPLLSVKVTFFGSGSVAVSVSHKICDIASLVTFFVK----- 164
QY 174 ACRNDPTEEMTAMNLDRTIIVYLENTYIGPEVDHQIVKADVAGDAVLTVPVSAWAF 233
Db 165 ---DWAT---TTAKGKSNSTI-EFAETTYIPPPSHMYEQFPSTDSNIT---SKYVL 213
QY 234 --FTFSPKAMSELK-DAATKTLDASTKFSVTDALSAFIKSA----- 273
Db 214 KRFVFEFSKIAELKHKAASESVPTVTRV---EAIMSLIMWCARNSSRSNLLIPROAVMW 269
QY 274 -----SRVRLERIDGSAPEFCRAVDARPAMGVSNYPGLLQNMVYHNSITIGETIA 323
Db 270 QAMDIRLIRIPSSVAPKDVIGNLQSGFSLKKDAESEFEI---PEIVATFRKNKERVNEMI 325
QY 324 NESIGATASRLSELDPASMRQTRGLATYLVHNNPDKSNVSLTAD-ADPSTSV---MLSS 379
Db 326 KESLQG-----NTIGQSLLSLMAETVSESTEIDRYIMSS 359
QY 380 WAKVGLWDYDGLGKGPETV---RRPIFEVESLMYFMPKKPDGFECAALSDEDM 436
Db 360 WCRKPFYEVDF--GSGSPVWVGVSHTIYDNMVGVLIDSKEGDG-VFAMTSLPEEDMSV 416
QY 437 LKADKEWTKYA 447
Db 417 FVDDQELLAYA 427

RESULT 11
US-09-457-046B-68
; Sequence 68, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 68
; LENGTH: 439
; TYPE: PRN
; ORGANISM: Catharanthus roseus
US-09-457-046B-68
```


Query Match 5.4%; Score 125.5; DB 3; Length 439;
Best Local Similarity 20.5%; Pred. No. 0.0003;
Matches 95; Conservative 75; Mismatches 193; Indels 101; Gaps 23;

QY 18 SIY---TQISLAYPVSDSSQYPTVTFBQGL-KRFSEAVPVWVAGQVKAEGISEGNTGTS 73
DB 39 NIYQTCVSVGFYENPDGIEISTIREQLQNSLTKTLVSVYPAGKVVKNDYTHCNDGIE 98
QY 74 FIVFPEDVRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPKTLPIGPTGDDP 133
DB 99 FV---EVRIRCRMNDI-----LKYELSYARDLVLPKRV-----VGSDET 136
QY 134 KPVIILQNFQKGLILTVNGQHGAMDVMGQDAVIRLLSK-----ACRNDPFTTEEWMTAM 188
DB 137 TAIQVLS-HFDCCGLAVAGISH-----KVADGGTIAFMKOWAASAC-----YL 180
QY 189 NLDKRTIVPYLENTYTGPEVDHQIVKADVAGDAVITPVSAWA---FFTFSPKAMSELKD 246
DB 181 SSSHVPTPLLVGDSIFPPQDNIIICQ-----FPTSNCVKEKTFIPPPPAIEKLEK- 230
QY 247 AATKTLDASTKVFSTDDALSAPTIWKA-----SRVLERIDGSAPTEFCRAVDARPMGV 301
DB 231 --SKAVEFGIEKTRVEVLTAFLSRCATVAGKAAKNNNGQSLPPFVLQAINLRPIL 288
QY 302 SNNYPGLQNMTHNSTIGETIANESLG-----ATASRLRSELDPSMRQRTGLA----- 351
DB 289 PQNSVGNLVSII-YFSRTIKE--NDYLNEXEYTKLVINELKE-----KQIKNLSREKL 339
QY 352 TYLHNNPD-----KSNVSLTADAPSTSVMLSSWAKVGLWMDYDFGLGKGPVTRRPPIF 405
DB 340 TYVAQMEEFVKSLEKFEIDISNFLDID---AYLSDSWCRPFYVDVF--GWGKPIWV--CLF 392
QY 406 EPVESLMYFMPKPDGE---FCAALSRLDEMDRLKADKEWTKY 446
DB 393 QPYIKNCVMMDPYFGDDYDYGIAIVSFQEKMSAFEKNEQLQF 436

RESULT 12
US-09-457-046B-73
; Sequence 73, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-73

Query Match 5.3%; Score 124; DB 3; Length 445;
Best Local Similarity 19.6%; Pred. No. 0.00044;
Matches 99; Conservative 79; Mismatches 176; Indels 126; Gaps 23;

QY 20 YTOISLILPYVSDSSQ---YPTIVSTFBQGL-KRFSEA-VPW---VAGQVKAEG-----ISE 67
DB 37 HTGAVLIYKQPDNEDNIHPSSSMYFDANILIEALSALVPFYPMAGELKINGDRYBIDC 96
QY 68 GNTGTSTIVPEEDVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPKTLPIGPG 127
DB 97 NAEALPV---EASSSHVLEDFG--FRPNDE-LHRVMVPTCDYSKGI----- 138
QY 128 TGPDDPKPVILLQL-NFTKGLILTVNGQHGAMDVMG-----QDAV 167
DB 139 ----SSPFLMVQLTRFCGVSIGFAGHHVCDGMHAFENNSWARIKALLPALEFVH 194
QY *168 IRLSKACRNDPFTTEEWMTAMNLDKRTIVPYLENTYTGPEVDHQIVKADVAGDAVITPV 227

DB 195 DRYLHLRPRNP---QIKYSHSQFEFFVPSLPNELLGK-----T 231
QY 228 SASWAFFTSPKAMSELKDAATKTLDAS--TKFVSTDDALSAPFIWKSASRVRLERIDGSA 285
DB 232 NKSQTLFILSRQINWLK---QKLDLSNNTTFLSTYEVVAHVWRSVSKAR--GLSDHE 285
QY 286 PTEFCRAVDARPA---GVSNNYPGLLQNMTHNSTIGETIANESLGATASR----- 333
DB 286 EIKLIMPVDGRSRINPSPKGYCGNVFLAVCTATVGDLSCNPLTDTAGKVOEALKGLD 345
QY 334 ---LRSELDPSMRQRTGLATVYLNHNPDKSNVSLTADADPSTSVMLSSWAKVGLWMDYDF 390
DB 346 DDYLRSAIDHTESKP---GLPVEYMGSPKTLV-----PNVLVNSMGRIPYQAMDF 393
QY 391 GLGLGKGPETVRRPIFPFVESLAMY-----FMPKKEP-DGEFCAALSRLDEMDRLK 438
DB 394 GWG-----SPTFFGIGNIFVDGQCFILPSRDEGSGMTLAINLFPSSHLRSEK 439

RESULT 13
US-09-457-046B-66
; Sequence 66, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Clarkia breweri
US-09-457-046B-66

Query Match 5.2%; Score 122; DB 3; Length 433;
Best Local Similarity 20.3%; Pred. No. 0.00067;
Matches 97; Conservative 64; Mismatches 196; Indels 122; Gaps 19;

QY 17 LSIYTOISLILPYVSDSSQYPTI-----VSTFQGLKRFSEAVPVWVAGQVKAEGISEGN 69
DB 26 LSLLDQIQIPFYVGLIFHYETLSDNSDITLSKLESSLSETLTLYHYHAGY----- 76
QY 70 TGTSTIVPEEDVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENI-----IAPRKT 122
DB 77 NGTDCVIECND-----QGI---GIVETAFDELHQLGELLESNNL 115
QY 123 PIGPG--TGPDDPKPVILLQLNFIK--GGLILTVNGQHGAMDVMGQDAVIRLLSKACRNDP 179
DB 116 LVGLSGFLSETETPPPLAAIQLNMFKCGLVIGAQFNHIIIGDMFTMTFMSWAKACR-- 172
QY 180 PTEEWMTAMNLDKRTIVPYLENTYTGPEVDHQIVKADVAGDAVITPVSAWAFFTSPK 239
DB 173 VGIKEVAHPTFGLAPLMPKSAKVLNIPPPSPFEGVKF-----VSKR---FVFN 218
QY 240 AMSCLKDAATK-----TLDASTKVFSTDDALSAPFIWKS----- 272
DB 219 ATRLRKEATEEDGDDGDDQKKRPSRVLDVITAFPLSKSLIEMDCAKKEQTKSRPSLAVHM 278
QY 273 ---ASRVRLERIDGSAPTEFCRAVDARPMGVSNYPGLLQNMTHNSTIGETIANESLGA 329
DB 279 MNLKRKTKL-ALENDVSGNFFIVVNAESKITVAPKITDLETSL---GSAOGEIISKVAKV 334
QY 330 TASRLRSELDPSMRQRTGLATVYLNHNPDKSNVSLTADADPSTSVMLSSWAKVGLWMDYD 389
DB 335 DDAFVSSVMLNSVRE-----FYEWGKGEKNVFL-----YTSRCRPFLEVD 377
QY 390 FGLGL-GKPEVTRRPIFPFVESLMYFMPKPDGEFCAALS--LRDEMDRLKADKEWTKY 446
DB 378 FGWGIPLSIVDTAVPF-----GLIVLMDAPAGIACVACLSLSEHMDIQOHHQLLSY 431

RESULT 14

US-09-457-046B-22
; Sequence 22, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-22

Query Match 5.2%; Score 121.5; DB 3; Length 306;
Best Local Similarity 20.7%; Pred. No. 0.00042;
Matches 59; Conservative 44; Mismatches 113; Indels 69; Gaps 10;
QY 135 PVILLQLNFIKGLLITVNGOHGMDVMVQDAVIRLLSKACRNDPFTBEETAMNLDKRT 194
DB 64 PLLAVQATKLDGIALATVNHAVADATSVWHFISSWAQLCK-----EPS 108
QY 195 IVPYLENY-----TIGPEVDHQIVKADVAGDAV-----LTPVSASWAFFTFSPKAMSE 243
DB 109 NIPLPLHTRCFTTISP-----IKLDIQSSTTTESIDNFPPLTEKIHFSKTIISR 162
QY 244 LKDAATKLDASTREKVSDDALSARIWKSASRVRLERIDGSAPTFCRAVDARPAAM--GV 301
DB 163 LKBEAMEACKSISISSFQALCGHLWQSITRAR--GLSPSEPTTIKIAVNCRPIVPPPL 220
QY 302 SNYPGLLQNNMTYHNSTIGEIANESLGATA-----SRLSELDPASMRQTR 348
DB 221 PNVYFGNAVQVVDVTMTTELLGNG-GACAAILLHQKISAHQDTQIRAEILD----- 270
QY 349 GLATYVHNPNKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLG 393
DB 271 -----KPKK--IVHTNNLIPCNIIAMAGSPRPPIYNNDFGNG 305

RESULT 15

US-09-457-046B-63
; Sequence 63, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-63

Query Match 5.2%; Score 121.5; DB 3; Length 482;
Best Local Similarity 19.5%; Pred. No. 0.00091;
Matches 99; Conservative 76; Mismatches 204; Indels 129; Gaps 21;
QY 9 TLGQLPGLLSIYTOISLXPVSDSQYPTIYSTFEQGLKRFSEAVPWVAGQVKAEG----- 64
DB 30 SVSDLPMLSCHYIKGCLUF--TCPNLPALSLHLKHSLSITLTHFPPLAGRLSTSSSGHV 88
QY 65 -ISEGNTGTSE-----IVPFEDVRVVVKDLRDDPSAPTIEGMEKAGYPMAFM 111
DB 89 FLTCDNAGADFVFAQAKSIHVSVDVIAGIDVPD--VVKFEFTYDRAVSVEGHN----- 138

QY 112 DENIIAPRKTLPIGPGTGDDPKPVILLQLNFIKGLLITVNGOHGMDVMVQDAVIRLL 171
DB 139 -----RPI LAVQVTEINDGVFIGSVNHAVTDGTSLNWFI----- 173
QY 172 SKACRNDPFTBEETAMNLDKRTIIVPYLENYITIGPEVDHQIVKADVAGDAVLTVPVSASW 231
DB 174 -----NTFAEVSRGAKNVTQPDFT-RESVLISPAV-----LKVP-QGPKVTFDENAPL 221
QY 232 --AFTTSPKAMSELKDAATKTL----- 252
DB 222 RERIFSFRESIQELKAVVNKKKWLTVNGEIDGVVELLGKQSNDKLNGKENGILTEMLFS 281
QY 253 -----DASTKVFSTD-----DALSARIWKSASRVRLERIDGSAPTFCRAVDARPAWGSN 303
DB 282 LFGNRDAVSKPVAVEISSFQSLCALLWRAITRAR--KLPSSKTTTTFRMAVNCRHLSPKL 339
QY 304 N---YPGLLQNM-TVHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLHNPD 359
DB 340 NPEYFGNAIQSVTPF--ATAAEVLSRDLKWCADQLNQSV-AAHQDGRIRSVVADWEANP- 395
QY 360 KSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLGKPKETVRRPIFEFVESLMIYFMP-KK 418
DB 396 --RCFPLGNAD-GASVTMGSSSPRPMPYDNDP--GWRPVAVRSGRSNKEDGKISAFPGR 450
QY 419 PDGEFCAALSRLDEDMORLKADKEWTKY 446
DB 451 GNGTVDLEVVLSPETMAGIESDGEFMRY 478

Search completed: February 7, 2004, 23:48:38
Job time : 73 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 7, 2004, 23:46:34 ; Search time 249 Seconds

(without alignments)

379.243 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAFKIQDITGLQGLLSIY.....EDMDLXADKWKYKQVVG 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2334	100.0	451	14	US-10-074-279-6	Sequence 6, Appli
2	1860.5	79.7	459	14	US-10-074-279-2	Sequence 2, Appli
3	962.5	41.2	474	14	US-10-074-279-8	Sequence 8, Appli
4	170.5	7.3	436	14	US-10-078-929-64	Sequence 64, Appli
5	168.5	7.2	446	14	US-10-078-929-52	Sequence 52, Appli
6	161	6.9	439	14	US-10-078-929-60	Sequence 60, Appli
7	144	6.2	431	14	US-10-078-929-200	Sequence 200, App
8	142	6.1	448	10	US-09-866-572A-56	Sequence 56, Appli
9	142	6.1	448	10	US-09-866-570A-56	Sequence 56, Appli
10	142	6.1	448	12	US-10-166-984-56	Sequence 56, Appli
11	142	6.1	448	15	US-10-166-984-56	Sequence 56, Appli
12	141.5	6.1	436	10	US-09-866-572A-62	Sequence 62, Appli
13	141.5	6.1	436	10	US-09-866-570A-62	Sequence 62, Appli
14	141.5	6.1	436	12	US-10-166-984-62	Sequence 62, Appli
15	141.5	6.1	436	15	US-10-166-984-62	Sequence 62, Appli

16	132	5.7	439	10	US-09-866-572A-28	Sequence 28, Appli
17	132	5.7	439	10	US-09-866-570A-28	Sequence 28, Appli
18	132	5.7	439	12	US-10-166-984-28	Sequence 28, Appli
19	132	5.7	439	15	US-10-166-984-28	Sequence 28, Appli
20	130.5	5.6	451	10	US-09-866-572A-69	Sequence 69, Appli
21	130.5	5.6	451	10	US-09-866-570A-69	Sequence 69, Appli
22	130.5	5.6	451	12	US-10-166-984-69	Sequence 69, Appli
23	130.5	5.6	451	15	US-10-166-984-69	Sequence 69, Appli
24	126.5	5.4	435	10	US-09-866-572A-60	Sequence 60, Appli
25	126.5	5.4	435	10	US-09-866-570A-60	Sequence 60, Appli
26	126.5	5.4	435	12	US-10-166-984-75	Sequence 75, Appli
27	126.5	5.4	435	15	US-10-166-984-75	Sequence 75, Appli
28	125.5	5.4	439	10	US-09-866-572A-68	Sequence 68, Appli
29	125.5	5.4	439	10	US-09-866-570A-68	Sequence 68, Appli
30	125.5	5.4	439	12	US-10-166-984-68	Sequence 68, Appli
31	125.5	5.4	439	15	US-10-166-984-68	Sequence 68, Appli
32	124	5.3	445	10	US-09-866-572A-73	Sequence 73, Appli
33	124	5.3	445	10	US-09-866-570A-73	Sequence 73, Appli
34	124	5.3	445	12	US-10-166-984-73	Sequence 73, Appli
35	124	5.3	445	15	US-10-166-984-73	Sequence 73, Appli
36	122	5.2	433	10	US-09-866-572A-66	Sequence 66, Appli
37	122	5.2	433	10	US-09-866-570A-66	Sequence 66, Appli
38	122	5.2	433	12	US-10-166-984-66	Sequence 66, Appli
39	122	5.2	433	15	US-10-166-984-66	Sequence 66, Appli
40	121.5	5.2	306	10	US-09-866-572A-22	Sequence 22, Appli
41	121.5	5.2	306	10	US-09-866-570A-22	Sequence 22, Appli
42	121.5	5.2	306	12	US-10-166-984-22	Sequence 22, Appli
43	121.5	5.2	306	15	US-10-166-984-22	Sequence 22, Appli
44	121.5	5.2	482	10	US-09-866-572A-63	Sequence 63, Appli
45	121.5	5.2	482	10	US-09-866-570A-63	Sequence 63, Appli

ALIGNMENTS

RESULT 1

US-10-074-279-6
; Sequence 6, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-10-074-279-6

Query Match 100.0%; Score 2334; DB 14; Length 451;

Best Local Similarity 100.0%; Pred. No. 3.7e-222;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFKIQDITGLQGLLSIYQTISLLYPVSDSSQYPTIVSTFQGLKRFSEAVPWAGQV 60

Db 1 MAFKIQDITGLQGLLSIYQTISLLYPVSDSSQYPTIVSTFQGLKRFSEAVPWAGQV 60

QY 61 KARGISEGNTGTGTFIVPFEDVPRVVKDLRDDSDSAPTIEGMRKAGYPMAMFENITAPRK 120

Db 61 KARGISEGNTGTGTFIVPFEDVPRVVKDLRDDSDSAPTIEGMRKAGYPMAMFENITAPRK 120

QY	121	TLPIGPGTGPDDPKPVIILLQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF	180
Db	121	TLPIGPGTGPDDPKPVIILLQNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF	180
QY	181	TEEMTAMNLRDKTIVPYLENTTIGPEVDHQIVKADVAGGDVAVLTPVGSASWAFFTFSPKA	240
Db	181	TEEMTAMNLRDKTIVPYLENTTIGPEVDHQIVKADVAGGDVAVLTPVGSASWAFFTFSPKA	240
QY	241	MSELKDAATKILDASTKFWSTDDALSAFTWKSASVRLERIDGSAPTFCRAVDARPAMG	300
Db	241	MSELKDAATKILDASTKFWSTDDALSAFTWKSASVRLERIDGSAPTFCRAVDARPAMG	300
QY	301	VSNNPGLLQNNYTHNSTTIGETANESLGATASRLSELDPASMRQTRGLAYLHNNPK	360
Db	301	VSNNPGLLQNNYTHNSTTIGETANESLGATASRLSELDPASMRQTRGLAYLHNNPK	360
QY	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPTVRRPIPEPVESLMYFMPKCPD	420
Db	361	SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPTVRRPIPEPVESLMYFMPKCPD	420
QY	421	GEFCAALSIRDEDMRLKADKEWTYQAYVG	451
Db	421	GEFCAALSIRDEDMRLKADKEWTYQAYVG	451

RESULT 2

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US-10-074-279-2
; Sequence 2, Application US/10074279
; Publication No. US2020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: prt
; ORGANISM: Fusarium sporotrichoides
US-10-074-279-2

```

Query Match	79.7%;	Score 1860.5;	DB 14;	Length 459;
Best local Similarity	77.6%;	Pred. No. 3e-175;		
Matches 349;	Conservative 50;	Mismatches 50;	Indels 1;	Gaps 1;
Qy	2	AFKIQDLTQLPGLLIYTIQISLLYPVSDSQSYPTIVSTTEQGLKRFSEAVPWVAGQVK	61	
Db	11	SFDIELDIIGQOPPLSIYTIQISLIVPVSQSYPTIVSTLEEGLKRLSQTFPPWVAGQVK	70	
Qy	62	ARGISEGNTGTSFIVPFEDVPRVVVKLDRDDPSAPFTIEGMRKAGPMAFMFENIIAPRKT	121	
Db	71	TEGISEGNTGTSKIIPIEETPLRVVKOLRDDSSAPFTIEGLRKAGPFLFEDENVVAPRKT	130	
Qy	122	LPIGGTGDDPKPVILLQLPFIKGLLIITVNGQHGAMDMVGODAVIRLLSKACRNDPPT	181	
Db	131	LAIQPGNGPNPKPVILLQLPFIKGLLIITVNGQHGAMDMTQODAIIRLLSKACNESFT	190	
Qy	182	EEEMTAMNLDKRTIIVPLENYTIQPEVDHQIVKADVAGDAVLTPVSAWAFPTFSPKAM	241	
Db	191	EEESAMNLDKRTVVPVPLENYKVGPELDHQIAKPAPA-GDAPPAPAKASWAFSTFPKAL	249	
Qy	242	SELKDAATKTLDASTKFFVSTDDALSAFTWKSASRVLERIDGSAFTFCRAVDARPMGV	301	

[illegible]

RESULT 3

```

RESULTS 3
US-10-074-279-8
; Sequence 8, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8

```

Query Match	41.2%;	Score	962.5;	DB	14;	Length	474;
Best Local Similarity	44.4%;	Pred. No.	2.9e-86;				
Matches	202;	Conservative	84;	Mismatches	158;	Indels	11;
Gaps							
Qy	6	QLDILGQLGGLSLTYTOISLLYPVSDSOYPTIVSTFEQGLKRSEAVPWVAGQVKAEGI	65				
Db	22	QLDILGQOPSLSKYUOTCSIRYVDPDSAHDHIVNTLGRLETLAKNQCWLAGNVVNSGA	81				
Qy	66	SEGNTGTSIVPFEDVRVVKVLDLDDPSAPTIRGMRKAGPYPMAMFDENIIAPRTKL-PI	124				
Db	82	DEGNTGTYRIVPSDKIP-LIVQDLRELLSAPTMDSLEKADFFIYMLDEKTFAPCMTINPP	140				
Qy	125	GPGTG-PDDPKPVILLQINFIKGGLITVNGOHGAMDMVGDAVIRLLSKACRNDPFTTEE	183				
Db	141	GNTTGMAAKSGPFVFAVQANFISGGVLLVTIVGQHIMDITGSEIINLNKSKHQPFPSDE	200				
Qy	184	EMTAMNLDKRTIVYLENYTTIGPEVD--HQIVKA--DVAGGDVAVLTPTS-ASWAFPTTSP	238				
Db	201	ELLIGNIDKSKIPLFDE-TWEPDTIIVHEIVETSRNTSGEEKQSCSSNSTVAVFESA	259				
Qy	239	KAMESLKDAANKTKLDAATKTFVSTDDALSAPTWKASASRVRLREIDGSAPTFCRAVDARPA	298				
Db	260	ISLQNLRIILAMQTCSTGTFKFTVSTDIVTAFATKWSVRARLGRLEKPKETKSNLGRAVDVRKR	319				
Qy	299	MGVSNNYPELLQNMYTHNSTTIGETANESLIGATASRLSELPLPA--SMRQRTREGLATYLHN	356				
Db	320	LGLPETYPELLVNMFTNFGSLKSLDKSLGLVLAQIRKRLDKPVDFLAINTCALATILLSR	379				
Qy	357	NPDKSNVSLTADADPSTSMVLSSWAKVGLWDYDFGLGLGCKBETVTRRRPTPEPVESLMYMP	416				
Db	380	CPDKTKVSIPOPIDITLIGIMVSSWAKVSLYDVDFNLGLGPKSVRRPPIFISLSTIYMP	439				

QY 417 KKPGEFCAALSLRDEMDRLKADKWKYQAYVG 451
Db 440 RSSRGEMVVALCLRKDWECNADKNWYNATHIG 474

RESULT 4

US-10-078-929-64
; Sequence 64, Application US/10078929
; Publication No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 64
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-078-929-64

Query Match 7.3%; Score 170.5; DB 14; Length 436;
Best Local Similarity 20.4%; Pred. No. 7.3e-08;
Matches 84; Conservative 61; Mismatches 158; Indels 109; Gaps 15;

QY 56 VAGQVKAEGISEGN-----TGTSFVPPFEDPRVVVVKDLRDDPSAPTIEGMKAGYPM 109
Db 78 LAERLGREG--EGRLOIDCNGEGALFVLARAPVAGEDLFGSGYEPSPE-IRRMFPVFA 134
QY 110 MFDENIIAPKTLPIGPGTGPDDPKPVILLQLNFIK--GGLILTVNGQHGAMDMVGQDAVI 168
Db 135 -----PSG-----DPPCHAMFQVTFKCGGVVLGTGHHVTMDGMAFHFI 176
QY 169 RL-----LSKACRNDPTEBEWMTAMNLDRTIVFYLYENYIGPEVDHQIVKADVAG 219
Db 177 QTWGLARGLSLSEACTSPPEFHDRTLRLARSPPR-----PEFEHPVVSAYLN 224
QY 220 GDAVLTPVSASWAFFTPSKAMSELKDAATKTLDASTKFYSTDDLSAFIWK----- 271
Db 225 G-----APRPVTRVYSVSKLLADIKSRCAPG-----VSTYGAVTAHLWRMCVARGL 273
QY 272 ---SASRVRL-----ERIDGSAPTEFCRAVDARPAMGVSNYPGLLQNMVTHNSTIGEIA 323
Db 274 APGSDITFLVPANIRHLRPLPROQFGNAIVRDLVTVK-----VGDVL 317

QY 324 NESLGATASRLRSSELDPASMRQRTGRGLATYHNNPDKSNVSLTADADPSTSVMLSSWAKV 383
Db 318 SQPLGYVADTIRKAVDHD-DAYTRSDVILEVESEKGSQAARQLMPESDLWVVSWLGM 376
QY 384 GLWDYDFGLGLGKPEVTVRPIFEPPVESIMYFMPKKPDGEFCAALSLRDEMD 435
Db 377 PMYDADEFWGAPR-----FVPAQMFSGTGATYYVTORGADRD 412

RESULT 5

US-10-078-929-52
; Sequence 52, Application US/10078929
; Publication No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 52
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Zea mays
US-10-078-929-52

Query Match 7.2%; Score 168.5; DB 14; Length 446;
Best Local Similarity 21.8%; Pred. No. 1.2e-07;
Matches 98; Conservative 63; Mismatches 177; Indels 111; Gaps 21;

QY 69 NTGTSIVPPEDPRVVVVKDLRDDPSAPTIEG-----MRKA-----GYMA-- 109
Db 24 NSGFDLWVFRFHTPSVYF--FRREDADGNLAGADGSFFDGMRRRLAEALVFPFMAGR 82
QY 110 -----MFDE-----NIAP-----RKTLPFGTGPDDPKPV 136
Db 83 LARDEGRVEIDCNAVGVLFQEADADPATIDYDGFAPTWELKRLIPTVDTDDISSFPL 142
QY 137 ILLQLNFIK--GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPPTTEEMTAMNLDKRTI 195
Db 143 LVILQVTHFGGVAIGVGMQHHVADGFGSLHFLINSWADLCRGVPI-----AV 189
QY 196 VPVLENYTIG-----PEVDHQIVKADVA--GDAVLTPVSA-----SWAFTTFSPKAM 241

Db 190 MPFIDRSLRLRDPPTPAYPHIEYQAPAMLEPPEQAAALTSKPAATPTTAVAFKLSRAEL 249
 QY 242 SELKDAAYTKTLDASTKFSVSTDDALSAFTWKSASRVRLERIDGSAPEFCRAVDAPAMGV 301
 Db 250 VRLR-SQVFAEGAPRF-STYAVLAHVWRCSLAR--GLPADQPTKLYCATDGRQL-- 303
 QY 302 SNNYP---GLQNNYTHNSTTGEIANESLGAT--ASRLRSELDPASMRQRTGLATYLH 355
 Db 304 ---QPLPREGYGNVIFTATPLANAGTVTAGVAGASVIOAALDRMD-DGYCRESALDYLE 359
 QY 356 NNPDKSNVSLTADADPSTSVMLSSNAKVLGWDYDFGLGKGPETVVRPIFE-----PVES 410
 Db 360 LQPDLSALVRGAHTFRCPCNLGLTSWVRLPIHDADFGWG-----RPVFMGPGGIAYRG 411
 QY 411 LMYFMPK-KPDGEFCAALSRLRDEMDRLK 438
 Db 412 LAFVLPSANRDGSLSVASLSQAEHMEKFR 440

RESULT 6
 US-10-078-929-60
 ; Sequence 60, Application US/10078929
 ; Publication No. US20020152497A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Miao, Guo-Hua
 ; APPLICANT: Falco, Saverio Carl
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Odell, Joan T.
 ; APPLICANT: Meyers, Blake
 ; APPLICANT: Thorpe, Catherine
 ; APPLICANT: Weng, Zude
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
 ; FILE REFERENCE: BB1357 US NA
 ; CURRENT APPLICATION NUMBER: US/10/078,929
 ; CURRENT FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: 09/566,394
 ; PRIOR FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: 60/133038
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: 60/133042
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: 60/133427
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133437
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133428
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133438
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133436
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/137667
 ; PRIOR FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 60
 ; LENGTH: 439
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-10-078-929-60

Query Match 6.9%; Score 161; DB 14; Length 439;
 Best Local Similarity 21.9%; Pred. No. 6.5e-07;
 Matches 99; Conservative 72; Mismatches 195; Indels 86; Gaps 20;
 QY 21 TQISLLYPVSDSSQPTIVSTFEQGLKRFSEAVWAGVQKAEGLSGNTGTSPFVFPED 80
 Db 25 SNVDLVVVP---NFHTPSVYFTRPNGVSNFFDA-----KWKKEALSK-----VLVDFYP 69
 QY 81 VPRVVVKDLRDDPSAPTI-----EGWR--KAGYPMAMFENIIAP-----RKTLPFGPGTGP 130

Db 70 ---MAARLRDDGRVEIYCDAGQVLFVEAETTTAAIEDFGDFSPTELEQLIPSVDSAG 126
 QY 131 DDPKPVILLQALFIK-GGILLTVNGOHGAMDMVGQDAVIRLLSKACRNDPPFTEEMTAMN 189
 Db 127 IHSYELLVLQVTFYKCGGVSGLVGHQHVADGASGLHFINAWSDVAR-----G 174
 QY 190 LDRKTIYPVLENYTIG-----PEVDHQIVKADVA-----GGDAVLTPVSAS 230
 Db 175 LD-ISLPPIDRTLLRARPPPLPVFDHIEYKPPATKTTPLQPSKPLGSDSTAVAVST- 232
 QY 231 WAPFTFSPKAMSELKDAATKTDASTKFSVSTDDALSAFTWKSASRVRLERIDGSAPEFC 290
 Db 233 ---FKLTRDQLSLTKGKSE--DGNITISYSSEMLAGHVWRSVCKAR--ALPDDQTKLY 285
 QY 291 RAVDARPA--GVSNYPGLQNNYTHNSTTGEIANESLGATASRLRSELDPASMRQRT 348
 Db 286 IATDGRARLQPPPLPHGYFNGVIFTTTRIAVAGDLMSKPTWYAAASRHDALIRMD-NEYL 344
 QY 349 GLATYILHNNPKSNVSLTADADPSTSVMLSSNAKVLGWDYDFGLGKGPETVVRPIFE-- 406
 Db 345 SALDYLELQPDLSKLVRGATFRCPCNLGLTSWVRLPIHDADFGWG-----RPIFMGP 396
 QY 407 ---PVESLMYFMPKPKP-DGEFCAALSRLRDEMD 434
 Db 397 GGIAYEGLSFIIPSTNDGSLSLAIALPPEQM 428

RESULT 7
 US-10-078-929-200
 ; Sequence 200, Application US/10078929
 ; Publication No. US20020152497A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Miao, Guo-Hua
 ; APPLICANT: Falco, Saverio Carl
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Odell, Joan T.
 ; APPLICANT: Meyers, Blake
 ; APPLICANT: Thorpe, Catherine
 ; APPLICANT: Weng, Zude
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
 ; FILE REFERENCE: BB1357 US NA
 ; CURRENT APPLICATION NUMBER: US/10/078,929
 ; CURRENT FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: 09/566,394
 ; PRIOR FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: 60/133038
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: 60/133042
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: 60/133427
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133437
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133428
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133438
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/133436
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 60/137667
 ; PRIOR FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 208
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 200
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Ipomoea batatas
 US-10-078-929-200

Query Match 6.2%; Score 144; DB 14; Length 431;
Best Local Similarity 24.6%; Pred. No. 3e-05;
Matches 84; Conservative 48; Mismatches 153; Indels 56; Gaps 17;

QY 119 RKTLPICGPGTGPDPKPVILLQLNFIK--GGILITVNGQHGAMDMVGQDAVIRLLSKACRN 177
DB 120 RKFTPTVDTSGDIESSFFLIIFOVTRFKGCGVCLGTGVFHTLSGVSLSLHINTWSDMARG 179

QY 178 -----DFTTEEMTAMNLDKRTIIVYLEN--YTTGPEVDHIOVKADVAGDAVLTPTVSAS 230
DB 180 LSWAIPFFIDRTLLRA---RDPPTPAFEHSEYDQPKL--KSVPEKRGSS-----SAS 227

QY 231 WAFPTSPKAMSELKDAATKTLASTKFSVDDALSAFIWKSASRVRLERIDGSAPTEFC 290
DB 228 TTMKLTPEQLALK--TKSKHEG-----STYELAHNIWCAKAR--GLTDDQATKLY 278

QY 291 RAVDAR-----PAMGVSNYPGLLQNMVTHNSTI---GEIANESLGATASRLRSELDPASM 343
DB 279 VATDGRSLCPPLP-----PGYLGNNVVTATPMAESGELQSEPLTNSAKRIHSALSAMD- 332

QY 344 RQTRGLATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKDETVRRP 403
DB 333 DEYLSALDFLECCPDLSKLIRGNSYFASPNLNINSWTRFLPVHESDFGWG-----RP 384

QY 404 I-PEPV---ESLMYEMPK-KPDGEFCAALSRLDEDMRLK 438
DB 385 IHMGPACLIEGTVIILPSPNKORTLSLAVCLDAEHMPLFK 425

RESULT 8
US-09-866-572A-56
; Sequence 56, Application US/09866572A
; Patent No. US20020138859A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/866,572A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/457,046
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-866-572A-56

Query Match 6.1%; Score 142; DB 10; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

QY 5 IQDITLQGLPGLLSIYTOISILYVPVSSOVPTTVSTFEOGLKRFSEAVPWAGOVKAEG 64
DB 35 LQLSVDRLPOMKFAFSAVLVYNASHSIFANPAQIIROALSKVLYQYPAFAGRIQKE 94

QY 65 ISE-----GNTGTSFIVPFEDVPRVVVKDLRDPDSAPTIEGMRKAGYPMAFMFENIIAPR 119
DB 95 NEELEVECTEGALFVEALVNDLSVLRLD-----DAQNASYEQLLF-----136

QY 120 KTLPIGCTGPDGPKPVILLQLNFIKGLILITVNGQHGAMDMVGQDAVIRLLSKACRND- 178
DB 137 -SLP--PNIQVQDLHLPLIQVTRFTCGGVVGVGFHGGICDARGGTQFLOGLADMARGT 193

QY 179 -PTEEBEMTAMNLDKRTIIVP-----YLENYITIGPEVDHIOVKADVAGDAVLTPTVSASWAF 233
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKG--LIRQPLKLD-----EIQAS 235

QY 234 FTSPKAMSELKDAATKTLASTKFSVDDALSAFIWKSASRVRLERIDGSAPTEFCRAV 293
DB 236 FTINSEIINIKQC---VIEECNEIFSAFVWVLTW--IARTKAFQIPHNNVMMFLGM 290

QY 294 DARPAMGVSNYPGLLQNMVTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PELPGK--YYGNAIGTSCVNIENQDLSRSLRAYMITKSKLIPIEN 343

QY 345 QRTREGATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EEIKHENVVFGDWRRLGFHEVDFGSG 383

RESULT 10
US-10-166-984-56
; Sequence 56, Application US/10166984
; Publication No. US20040005562A9
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 4630-62267
; CURRENT APPLICATION NUMBER: US/10/166,984
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/866,570

QY 294 DARPAMGVSNYPGLLQNMVTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PELPGK--YYGNAIGTSCVNIENQDLSRSLRAYMITKSKLIPIEN 343

QY 345 QRTREGATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EEIKHENVVFGDWRRLGFHEVDFGSG 383

RESULT 9
US-09-866-570A-56
; Sequence 56, Application US/09866570A
; Patent No. US20020168745A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/866,570A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/457,046B
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-866-570A-56

Query Match 5.1%; Score 142; DB 10; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

QY 5 IQDITLQGLPGLLSIYTOISILYVPVSSOVPTTVSTFEOGLKRFSEAVPWAGOVKAEG 64
DB 35 LQLSVDRLPOMKFAFSAVLVYNASHSIFANPAQIIROALSKVLYQYPAFAGRIQKE 94

QY 65 ISE-----GNTGTSFIVPFEDVPRVVVKDLRDPDSAPTIEGMRKAGYPMAFMFENIIAPR 119
DB 95 NEELEVECTEGALFVEALVNDLSVLRLD-----DAQNASYEQLLF-----136

QY 120 KTLPIGCTGPDGPKPVILLQLNFIKGLILITVNGQHGAMDMVGQDAVIRLLSKACRND- 178
DB 137 -SLP--PNIQVQDLHLPLIQVTRFTCGGVVGVGFHGGICDARGGTQFLOGLADMARGT 193

QY 179 -PTEEBEMTAMNLDKRTIIVP-----YLENYITIGPEVDHIOVKADVAGDAVLTPTVSASWAF 233
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKG--LIRQPLKLD-----EIQAS 235

QY 234 FTSPKAMSELKDAATKTLASTKFSVDDALSAFIWKSASRVRLERIDGSAPTEFCRAV 293
DB 236 FTINSEIINIKQC---VIEECNEIFSAFVWVLTW--IARTKAFQIPHNNVMMFLGM 290

QY 294 DARPAMGVSNYPGLLQNMVTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PELPGK--YYGNAIGTSCVNIENQDLSRSLRAYMITKSKLIPIEN 343

QY 345 QRTREGATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EEIKHENVVFGDWRRLGFHEVDFGSG 383

Db 227 KIKKLAKASRL-----VKNPTRVAVTALFWRCVTKV--SRLSSLTP-----RTSVLIQILV 277

Qy 300 GVSNNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTFGLATYILHNNPD 359

Db 278 NLRGKVDLSICENTIGNMLSLMILKNEE--AAIERIQDVVDEI---RRAKEIFSLNCKEMS 332

Qy 360 KSNVSLTADADPSTV-----MLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVE 409

Db 333 KSSSRIFELLEIEIGKVGGRGNEMDLWMSNSWCKLGLYDADF--GWGKPVVVTGRTGTSHEK 390

Qy 410 SLMYFMPKKPDGEFCFAA--LSLRDEDMDRLKADKE 442

Db 391 NLMLLIDTK-DGEGIEAWITLTTEEQMSLFECDQE 423

Search completed: February 8, 2004, 00:12:21

Job time : 249 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:04:23 ; Search time 3189 Seconds
(without alignments)

10334.547 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacagct.....atggcagtagcttggttag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estm.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_estl.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663.8	49.0	899	12	BI949616
2	406	29.9	1055	12	BI947129
3	354.2	26.1	512	12	BI191800
4	351	25.9	508	12	BI191865

5	323.4	23.8	498	12	BI200717
6	317.6	23.4	499	12	BI191678
7	296.6	21.9	481	12	BI191864
8	278.4	20.5	514	12	BI192008
9	278	20.5	411	12	BI187781
10	273.4	20.2	448	12	BI201068
11	273	20.1	518	12	BI191997
12	268.4	19.8	457	12	BI187780
13	258	19.0	392	12	BI192452
14	254.8	18.8	423	12	BI192498
15	251.2	18.5	490	12	BI201353
16	247.4	18.2	374	12	BI187896
17	242.8	17.9	476	12	BI192381
18	234.4	17.3	401	12	BI188598
19	234.4	17.3	401	12	BI192451
20	233.4	17.2	348	12	BI191129
21	231.6	17.1	459	12	BI187539
22	231.2	17.1	393	12	BI188605
23	226.6	16.7	372	12	BI192380
24	223.8	16.5	336	12	BI191040
25	218.6	16.1	358	12	BI201146
26	217.2	16.0	435	12	BI187304
27	215.4	15.9	350	12	BI190499
28	206.6	15.2	330	12	BI191128
29	202	14.9	546	10	BF253868
30	196	14.5	385	12	BI189867
31	195	14.4	318	12	BI192335
32	187.6	13.8	303	12	BI188705
33	187.6	13.8	303	12	BI189964
34	187.6	13.8	304	12	BI190847
35	187.6	13.8	308	12	BI188363
36	187.6	13.8	308	12	BI190145
37	187	13.8	311	12	BI200611
38	170.4	12.6	373	12	BI190682
39	170.4	12.6	376	12	BI189442
40	170.4	12.6	380	12	BI190409
41	169.4	12.5	352	12	BI188631
42	169.4	12.5	352	12	BI201565
43	169.4	12.5	360	12	BI187939
44	169.4	12.5	361	12	BI201147
45	169.4	12.5	379	12	BI189968

ALIGNMENTS

RESULT 1
BI949616
LOCUS
DEFINITION
BI949616 899 bp mRNA linear EST 19-OCT-2001
HVSMEL10014017f Hordeum vulgare spike EST library HVCDNA0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSMEL10014017f, mRNA sequence.

ACCESSION
BI949616
VERSION
BI949616.1 GI:16291032
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 899)

REFERENCE
AUTHORS
Wing, R., Muehlbauer, G.J., Close, T.J., Kleinbols, A., Wise, R., Heinen
S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library

TITLE
JOURNAL
COMMENT
Unpublished
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288

Fax: 864 656 4293
 Email: rwing@clermson.edu
 Total hq bases = 598
 Seq primer: AATTAAACCTCACTAAAGGG
 High quality sequence stop: 755.
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="Morex"
 /db_xref="taxon:112509"
 /clone="HVSME1001401F"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /clone_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI. Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the RJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"
 BASE COUNT 223 a 262 c 204 g 209 t 1 others
 ORIGIN

Query Match 49.0%; Score 663.8; DB 12; Length 899;
 Best Local Similarity 95.8%; Pred. No. 6.9e-178;
 Matches 724; Conservative 0; Mismatches 28; Indels 4; Gaps 4;
 QY 1 ATGGCTTCAAGATACAGCTCGACACCTCGGCAGCTACGAGGCTCTTTCGATCTAC 60
 DB 110 ATGGCTTCAAGATACAGCTCGACACCTCGGCAGCTACGAGGCTCTTTCGATCTAC 169
 QY 61 ACCCAATACGTCCTCTACCCCGCTCTCGATTCCTCAATATCCCACTATTGTGAGC 120
 DB 170 ACCCAATACGTCCTCTACCCCGCTCTCGATTCCTCAATATCCCACTATTGTGAGC 229
 QY 121 ACCTTCGAGCAAGTCTTAAGCGCTTCTCGAAGCGCTCCGATCGGTCGAGCGCAGGTC 180
 DB 230 ACCTTCGAGCAAGTCTTAAGCGCTTCTCGAAGCGCTCCGATCGGTCGAGCGCAGGTC 289
 QY 181 AAAGCCGAGGCAATACGAGGGAACACAGGAACTCTTTATCGTCCCTTTTGAGGAC 240
 DB 290 AAAGCCGAGGCAATACGAGGGAACACAGGAACTCTTTATCGTCCCTTTTGAGGAC 349
 QY 241 GTTCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCAGCGCCACGATCAGGGT 300
 DB 350 GTTCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTCAGCAACCCAGATCAGGGT 409
 QY 301 ATGAGAAGCGCGGATACCTTATGGCGATGTTTGAAGAGAACATCATCGCGCCAGGAAG 360
 DB 410 ATGAGAAGCGCGGATACCTTATGGCGATGTTTGAAGAGAACATCATCGCGCCAGGAAG 469

QY 361 ACGTTACCTATTGGACCTGGTACTGTCCTCCGACGACCCAAAGCCCTGTAATTCATTGCGAG 420
 DB |||||
 QY 470 ACGTTACCTATTGGACCTGGTACTGTCCTCCGACGACCCAAAGCCCTGTAATTCATTGCGAG 529
 DB |||||
 QY 421 CTCAACTTCATCAAGGGCGGACTCATCTCATCTCAACGGACAGCAGCTGCTATGGAT 480
 DB |||||
 QY 530 CTCAACTTCATCAAGGGCGGACTCATCTCATCTCAACGGACAGCAGCTGCTATGGAT 589
 DB |||||
 QY 481 ATGGTAGGCCAAGATCGGTGATCGTCTACTCTCTCAAGGCGTGGCGTAACGACCCATTC 540
 DB |||||
 QY 590 ATGGTAGGCCAAGATCGGTGATCGTCTACTCTCTCAAGGCGTGGCGTAACGACCCATTC 649
 DB |||||
 QY 541 ACCGAAGAGGAATGACGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA 600
 DB |||||
 QY 650 ACCGAAGAGGAATGACGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA 708
 DB |||||
 QY 601 AACTATACGATTGGCCCGAGGTAGATCATCATGATTTCAAAGCTGATAGTGTGCTGGT 660
 DB |||||
 QY 709 AACTATACGATTGGCCCGAGGTAGATCATCATGATTTCAAAGCTGATAGTGTGCTGGT 768
 DB |||||
 QY 661 GAGCGTGT-TCTCAGCGCGTCAAGCTGAGCTGGCGCTTCTTCAATTCAGCCGCCAAGGC 719
 DB |||||
 QY 769 GTGACCGCTGTCTACCCCGTCAAGCTGAGCTGGCGCTTCTTCAATTCAGCCGCCAAGGC 827
 DB |||||
 QY 720 CATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCT 755
 DB |||||
 QY 828 CATGTCANAGCTC-AGGATGCTGTACCAAGACTCT 862
 DB |||||

RESULT 2
 BI947129
 LOCUS
 DEFINITION
 HVSME1003N10f Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HVSME1003N10f, mRNA sequence.
 BI947129
 BI947129.1 GI:16286403
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Hordeum.
 1 (bases 1 to 1055)
 WING, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D.
 Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library

Unpublished
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 total hq bases = 147
 Seq primer: AATTAAACCTCACTAAAGGG
 High quality sequence start: 5
 High quality sequence stop: 668.
 Location/Qualifiers
 1..1055
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Morex"
 /db_xref="taxon:112509"
 /clone="HVSME1003N10f"
 /tissue_type="Spike"
 /lab_host="TJC121"
 /clone_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"

FEATURES
 source

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the G1 Muehlbauer lab, spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT 300 a 313 c 227 g 215 t
ORIGIN

Query Match 29.9%; Score 406; DB 12; Length 1055;
Best Local Similarity 79.4%; Pred. No. 2.4e-104;
Matches 481; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 387 TCCGACGACCCAAAGCTGTAATTCATTTCAGCTCAACTTCATCAAGGCGGACTCAT 446
Db 1 TCCGACGACCCAAAGCTGTAATTCATTTCAGCTCAACTTCATCAAGGCGGACTCAT 60

QY 447 CCTCACTGTCAACGACGACGCTGTATGGATGTGGTGGCCAAAGATGGCGTATCCG 506
Db 61 GCTCACTGTCAACGACGACGCTGTATGGATGTGGTGGCCAAAGATGGCGTATCCG 120

QY 507 TCTACTCTCCAGGCGTGCCTGTAACGCCATTCACCGAAGAGAAATGACGGCCATGAA 566
Db 121 TCTACTCTCCAGGCGTGCCTGTAACGCCATTCACCGAAGAGAAATGACGGCCATGAA 180

QY 567 CCTCGATCGCAAGCATAGTTCCTTACCTTGAAAACTATACAGATGGCCCCGAGGTAGA 626
Db 181 CCTCGATCGCAAGCATAGTTCCTTACCTTGAAAACTATACAGATGGCCCCGAGGTAGA 240

QY 627 TCATCAGATTGTCAAAGCTGATGTAGTGTGGTGACGCTGTTCTCAGCGGTCAGTGC 686
Db 241 TCATCAAAATGTCAAACTGATGTAGTGTGGTGACGCTGTTCTCAGCGGTCAGTGC 300

QY 687 AAGTGGCGCTTCTTCATTCAGCCCAAGGCCATGTCAAGCTCAAGGATGTGCTAC 746
Db 301 AAATCTGGCGCTTCTTCATTCAGCCCAAGGCCCTGTCAAGCTTAAGATGTCTGCTC 360

QY 747 CAAGACTCTTGACGATCAACAAGTTCGTGTGATGACGATGCTCTTTTCGGCGTTTCAT 806
Db 361 CAAGAAATTTTAAAGCATTAACAAGTTCGTGTGATGACGATGCTCTTTTCGGCGTTTCAT 420

QY 807 CTGGAAATCGGCTCTCGGCTGCTTCGAAAGAAATCGATGGCTCTGCACCTACCGAGTT 866
Db 421 CTGGAAATCGGCTCTCGGCTGCTTCGAAAGAAATCGATGGCTCTGCACCTACCGAGTT 480

QY 867 CTCGCGTGTGTTGATGCTCGACGGCAATGGGTGTCTCGAAACAATACCGACGCTTCT 926
Db 481 GCAGCGTCAATTTAAAGCATTAACAAGTTCGTGTGATGACGATGCTCTTTTCGGCGTTTCAT 540

QY 927 TCAAAACATGACCTACCAACATTCGACCATTCGCGCAAAATCCCAACAGAGTCACTCGCGCG 986
Db 541 TCCGTAACACGCTTTTCCAAACGTAACCGACCGCGCAACGCGCATCCGTGTCTCTCGCGGGA 600

QY 987 AACAGC 992
Db 601 ACCAGC 606

RESULT 3 BI191800

LOCUS DEFINITION

BI191800 512 bp mRNA linear EST 10-JUL-2001
12f11fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 12f11fs 5', mRNA
sequence.

ACCESSION

BI191800 GI:14665479

VERSION

EST.

KEYWORDS

Fusarium sporotrichioides

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE

1 (bases 1 to 512)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand

AUTHORS

,M. and Roe,B.

TITLE

Analysis of a Fusarium sporotrichioides EST database

JOURNAL

Unpublished

COMMENT

Other ESTs: 12f11fs.f1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

871 8e-94 gi|437882[gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: T3

High quality sequence stop: 476.

Location/Qualifiers

1. 512

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clones="12f11fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed

cDNA library"

/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 130 a 153 c 121 g 107 t 1 others

ORIGIN

Query Match 26.1%; Score 354.2; DB 12; Length 512;

Best Local Similarity 82.8%; Pred. No. 8.8e-90;

Matches 407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACAGGCTCTCTTCGATCTACAC 62

Db 16 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTCTTTTCAATCTACAC 75

QY 63 CCAATCAGTCTCCTCTA CCCCCTCTCTGATTCCTCTCAATATCCCACTATTCTCAGCAC 122

Db 76 CCAGATCAGTCTCGTTTACCCCGTCTCTGATTCCTCTCCAGTATCCCACTATCTCAGCAC 135

QY 123 CTTTCGACGAGTCTTAAGCGTTCCTCCGAGCCGTCCTCCATGGTTCGAGGCGAGTCAA 182

Db 136 CTTTCGAGGAGCGCTAAAACGGCTCTCTCAAACTTCCCATGGTTCGCGGCGAGTCAA 195

QY 183 AGCCGAGGAGCATTTAGCGAGGAAACACAGAACTTCTTATCGTCCCTTTTTCAGACGT 242

Db 196 GACCGAGGAGCATTCAGCGAAGGAAACACAGAACTTCTCAAGATCATTTCCATATGAGGAGAC 255

QY 243 TCCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGGCGCCACGATCGAGGTAT 302

Db	256	ACCCGCTTGTGGTGAAGACCTCCGATGATGTTCTCAGCGCAACGATCAGGGTT	315
QY	303	GAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAAGAGAC	362
Db	316	GAGAAAGCGGGTTCCTCTTAGAGATGTTTGACGAGAACGTCGTCGCTCCGAGGAGAC	375
QY	363	GTTACTATTGGACTGGTGTGTCGCGAGACACCGCAAGCCGTGAATTCATTCAGCT	422
Db	376	ATTAGCTATCGACCTGGCAATGGCCCAACACCGCAAGCCGTGTGTTGCTATTGAGCT	435
QY	423	CAACTTCATCAGGGGGGACTCATCTCACTGTCAACGACAGCGGTGTATGGATAT	482
Db	436	CAACTTCATTAAGGGCGGACTCATCTCACTGTCAACGACAGCATGGTGCTATGGACAT	495
QY	483	GCTAGGCCCAAGATGC	497
Db	496	GACAGGACCAAGATGC	510
RESULT 4			
BI191865		508 bp mRNA linear	EST 10-JUL-2001
LOCUS		l3b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA	
DEFINITION		library Fusarium sporotrichioides cDNA clone l3b10fs 5', mRNA	
ACCESSION		BI191865	
VERSION		BI191865.1	GI:14665544
KEYWORDS		EST.	
SOURCE		Fusarium sporotrichioides	
ORGANISM		Fusarium sporotrichioides	
REFERENCE		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.	
AUTHORS		Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand ,M. and Roe,B.	
TITLE		Analysis of a Fusarium sporotrichioides EST database	
JOURNAL		Unpublished	
COMMENT		Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Farrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability. Included is the best homolog from a blastx search of Genbank nr 04-09-01 857 3e-92 gi 4378882 gb AAD197 (AF127176) trichothecene3-O-acetyltransfer Seq primer: T3 High quality sequence stop: 450.	
FEATURES		Location/Qualifiers	
source		1..508	
		/organism="Fusarium sporotrichioides"	
		/mol_type="mRNA"	
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		/db_xref="taxon:5514"	
		/clone="l3b10fs"	
		/cdna_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"	
		/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"	
BASE COUNT		129 a 151 c 122 g 106 t	
ORIGIN			
Query Match		25.9%; Score 351; DB 12; Length 508;	
Best Local Similarity		81.8%; Pred.No.7.2e-89;	
Matches 405; Conservative		0; Mismatches 90; Indels 0; Gaps 0;	
QY	3	GGCTTTCAGATACAGCTCGACACCTCGCGCAGCTACAGCGCTCCTTCGATCTACAC	62

DB	199	TTGAGAGAACCTCGCTTTGAAACCTTTTCAGAGATTTCGATCTTATTCGCCCAAGAAGCC	140
QY	1257	TGATGGCGAGTTCTCTGGCGGCGCTTCTCTGAGGATGAGGATATGGACCGATTGAAGGC	1316
Db	139	TGATGGGAGTTTACGGCGTCCAATTCTCTGAGGGATGAGGATATGGAGAGACTAAAGGC	80
QY	1317	GGATAAGAGTGGACCAAGTATGCCAGTACGTTGGTTAG	1356
Db	79	GGATGAGGATGGACAAAGTACGCAAGTATATTCGGTAG	40
RESULT 7			
BI191864/c			
LOCUS		481 bp	linear
DEFINITION		BI191864	EST 10-JUL-2001
		13b1018.fl	Fusarium sporotrichioides Tri 10 overexpressed cDNA
		library	Fusarium sporotrichioides cDNA clone 13b1018 3', mRNA
		sequence.	
ACCESSION		BI191864	
VERSION		BI191864.1	GI:14665543
KEYWORDS		EST.	
SOURCE		Fusarium sporotrichioides	
ORGANISM		Fusarium sporotrichioides	
		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
		Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.	
REFERENCE		1 (bases 1 to 481)	

AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished
COMMENT Other ESTs: l3b10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
745 4e-79 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransferase
Seq primer: M13-20
High quality sequence stop: 340.

FEATURES

source

1. 481
Location/Qualifiers

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="l3b10fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript"

; 3' end of cDNA cloned into XhoI site of pBluescript"

116 a 129 c 111 g 125 t

BASE COUNT**ORIGIN**

Query Match 21.9%; Score 296.6; DB 12; Length 481;

Best Local Similarity 80.5%; Pred. No. 2.2e-73;

Matches 347; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 926 TTCAAAACATGACCTACCACTCGACCATCGGCAATCGCAAGAGTCACTCGGCG 985

DB 481 TTCAAAACATGACCTACCACTCGACCATCGGCAATCGCAAGAGTCACTCGGCG 422

QY 986 CAACAGCATCAGCCCTTGGTTCAAGAACTCGACCCCGAGCATGCGCGCAACAAAGAG 1045

DB 421 CAACAGCATCAGCCCTTGGTTCAAGAACTCGACCATCGGCAATCGCAAGAGTCACTCGGCG 362

QY 1046 GTCTCGGAGTACCTGCAACAACCCGCAAGTCCCAAGTATCCCTGACCGCTGATG 1105

DB 361 CTCTTGGCGAGTACATGATGCGGCTGCTGCAAGTCAAGTCAAGTCAAGTCAAGT 302

QY 1106 CGGACCATCTACCGAGTCACTGAGTCTTGGGCAAGTGGGAGTCTGGGATTAAG 1165

DB 301 CGAATCGTCAAGCAGATCATGCTGAGTCTTGGGCAAGTGGGAGTCTGGGATTAAG 242

QY 1166 ACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTGAGCGGCCCAATCTTTGAGCTGTG 1225

DB 241 ACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTGAGCGGCCCAATCTTTGAGCTGTG 182

QY 1226 AGAGCTTGATGATCTTTATGCCCAAGAGCTGATGCGGAGTCTGCGGCGCTTCTC 1285

DB 181 AGAGCTTGATGATCTTTATGCCCAAGAGCTGATGCGGAGTCTGCGGCGCTTCTC 122

QY 1286 TGAGGATGAGGATATGACCGATTAAGCGGATTAAGGATGAGGATGAGGATGAGGAT 1345

DB 121 TGAGGATGAGGATATGACCGATTAAGCGGATTAAGGATGAGGATGAGGATGAGGAT 62

QY 1346 ACCTTGCTTAG 1356

DB 61 ATATTGGTAG 51

RESULT 8

B1192008

LOCUS

514 bp mRNA linear

EST 10-JUL-2001

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

l4c09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone l4c09fs 5', mRNA
sequence.

B1192008

B1192008.1

GT:14665687

EST.

Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; mitospore Hypocreales; Fusarium.

1 (bases 1 to 514)

Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand

M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

730 3e-77 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransferase

Seq primer: T3

High quality sequence stop: 476.

FEATURES

source

1. 514
Location/Qualifiers

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="l4c09fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript"

; 3' end of cDNA cloned into XhoI site of pBluescript"

135 a 162 c 112 g 105 t

BASE COUNT**ORIGIN**

Query Match 20.5%; Score 278.4; DB 12; Length 514;

Best Local Similarity 81.0%; Pred. No. 3.6e-68;

Matches 324; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 3 GGCTTTCAGATACAGCTCGACACCTCGGCCAGCTACCGAGGCTCTTTTCGATCTACAC 62

DB 115 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTCTTTTCAATCTACAC 174

QY 63 CCAATCAGTCTCTCTACCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTGACAC 122

DB 175 CCAGATCAGTCTCTGTTTACCCGCTCTCTGATTCCTCCAGTATCCCACTATGTCACAC 234

QY 123 CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAGCGCTCCCAAGGTCGACGCGCAGGTCAA 182

DB 235 CCTTGAGGAAGGCTTAAACGCTCTCTCAAACTTCCCATGGGTGCGGCGCAGGTCAA 294

QY 183 AGCGGAGGATTTAGCGAGGAAACACAGCACTCTCTTTATCGTCCCTTTTTCGAGGACGT 242

DB 295 GACCGAGGATTCAGCGAAGGAAACACAGCACTTCCAAATCATTCATATGAGGAGAC 354

QY 243 TCCTCGTGTGTAGTGAAGACCTCCCGATGATCTTCAGCGGCCCACTATGCGAGGTAT 302

DB 355 ACCCGCTCTGTGTGAAGACCTCCGTGATGATTCCTCAGCGCCACGATCGAGGTT 414

QY 303 GAGAAAGCGGATACCTATGCGATGTTTGAAGAGAAATCATTCGCGCCAGGAGAC 362

DB 415 GAGAAAGCGGTTTCCCTTAGAGATGTTTGAAGAGAGCTGCTCGCGAGGAGAC 474

QY 363 GTTACCTATTGACCTGTTACTGTCCTCCGAGGCCCAAG 402

Db 475 ATTAGTATCGGACCTGGCAATGGCCCAACGCCGAAG 514

RESULT 9

Bi187781

LOCUS

DEFINITION Bi187781 411 bp mRNA linear EST 10-JUL-2001
b2d04fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
sequence.

ACCESSION

VERSION Bi187781.1 GI:14661460

SOURCE

ORGANISM

Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 411)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
, M. and Roe, B.

TITLE

JOURNAL

COMMENT

Other ESTs: b2d04fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
591 4e-61 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3

High quality sequence stop: 307.

FEATURES

source

1. .411
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="b2d04fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 99 a 122 c 96 g 94 t

ORIGIN

Query Match 20.5%; Score 278; DB 12; Length 411;
Best Local Similarity 81.2%; Pred. No. 4.1e-69;
Matches 336; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 401 AGCTGTAACTTATTGACGCTCACTTTCATCAAGGCGGACTCATCTCACTGTCAAG 460

Db 1 AGCTGTGTGCTATTGCACTCACTTCACTTAAAGCGGACTCACTCACTCAAG 60

QY 461 GACAGCAGGTGCTATGATGATGTAGGCAAGATGCGGTGATCCGTTACTCTCAAGG 520

Db 61 GACAACTGCTGCTATGACATGACAGGCAAGATGCAATATTGCTTCTTCCNAGG 120

QY 521 CGTGGCGTAAGCCCATTCACGAGAGGAATGAGCGGCATGAACCTCGATCGCAAG 580

Db 121 CGTGGCGCAACGAATCATTCACGAGGAGGAATCTCGGCATGAACCTCGATCGCAAG 180

QY 581 CGATAGTTCCTTACCTTGAACCTATACAGTATGCGCCCGAGGTAGATCATCATGTGCA 640

Db 181 CGTATGTCCTCTCTTGAACCTATACAGTATGCGCCCGAGGTAGATCATCATGTGCA 240

QY 641 AAGCTGATGTAGTGTGTGAGCGCTTCTCTCAAGCGCGGTCAAGTGTGGCGGTCT 700

Db 241 AACCC--TGCGCTGTGGGACGCTCCACCGGACCGGCAAGGCAAGCTGGCGTCT 297

QY 701 TCACATTACGCCCAAGGCCAATGTGAGACTCAAGGATGCTGTACCAAGACTCTTGAGC 760
Db 298 TTTTCACTTCACTCCCAAGGCCCTCTCGAGCTGAAAGACGACGACCAAGACTCTTGAGC 357
QY 761 CATCAACAAGATTCGTTCGACTGACCATGCTCTTTCGGCGTTTCATCTGGAAT 814
Db 358 CGTGTCCAAAGTTTGTGTCAACTGATGCTCTTTCGGCGTTTATCTGGAAT 411

RESULT 10

Bi201068/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other ESTs: b2d04fs.f1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

694 4e-73 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: M13-20

High quality sequence stop: 303.

FEATURES

source

1. .448

Location/Qualifiers

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="04c12fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed

cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 107 a 126 c 101 g 114 t

ORIGIN

Query Match 20.2%; Score 273.4; DB 12; Length 448;

Best Local Similarity 79.9%; Pred. No. 8.8e-67;

Matches 322; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 954 CATCGCGGAATCGCAACGAGTCACTCGCGCAACAGCATACGGCTTCGTTCAAGT 1013

Db 448 CGTTCGCGGAATCGCAACGAGTCACTCGCGCAACAGCATACGGCTTCGTTCAAGT 389

QY 1014 CGACCCCGCGGATCGCGCGAGCAAGAGTCTCGCGACGTACTCGCAACACCC 1073

Db 388 CAACAGTATCGTTTCGCGAGCAACAGCTTTGGCGACGTATCATGCGCTGCC 329

QY 1074 CGACAAGTCAACGATATCCTGACGGCTGATCGGACCCATCTACCAGCGTCAATGCTGAG 1133

Db 328 TGACAAGTCAAGGCTCTCCTGACCGCGGATGCGATCGTCAAGCAGCATCATGCTGAG 269

QY 1134 TTCTTGGCGCAAGTGGGACTCTGGGATTCGACTTTGGGCTCGGACTGGTAAAGCCGA 1193

Db 268 TTCTGGCCCAAGTGGGATGCTGGAGATGACITTTGGTTGGAGTGGTAAAGCTGA 209
 Qy 1194 GACTGTGAGACGCCCAATTTTGGCTTTGAGAGCTTGATGATCTTTATGCGCCAGAA 1253
 Db 208 GAGTGTGAGAGACCTCGCTTTGAACCTTTGAGAGTTTGATGATCTTTATGCGCCAGAA 149
 Qy 1254 GCGTATGCGAGTCTGTGGCGGCTTTCTCTGAGGATGAGGATGATGACCGATTGAA 1313
 Db 148 GCGTATGCGGAGTTTACCGCGTCCATTTCTCTGAGGATGAGGATGATGAGAGACTAA 89
 Qy 1314 GCGGATAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
 Db 88 GCGGATAGGAGTGGACCAAGTACGCAAGTATATTTGGTAG 46

RESULT 11

Bi191997
 LOCUS 518 bp mRNA linear EST 10-JUL-2001
 DEFINITION 14b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 14b10fs 5', mRNA sequence.

ACCESSION Bi191997
 VERSION Bi191997.1 GI:14665676

KEYWORDS

SOURCE

ORGANISM

Fusarium sporotrichioides
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE

1 (bases 1 to 518)

AUTHORS

Ren.Q., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand M. and Roe.B.

TITLE

Analysis of a Fusarium sporotrichioides EST database

JOURNAL

Unpublished

COMMENT

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 712 3e-75 gi|4378882|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransfer
 Seq primer: T3
 High quality sequence stop: 484.

FEATURES

source

1. .518 Location/Qualifiers

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="14b10fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 137 a 162 c 112 g 107 t

ORIGIN

Query Match 20.1%; Score 273; DB 12; Length 518;
 Best Local Similarity 80.9%; Pred. No. 1.2e-66;
 Matches 318; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 3 GGCTTTCAAGATACAGTTCGACACCTCGGCCAGCTACCGGCTCTCTTGGATCTACAC 62

Db 126 GTCTTTTGACATAGAGTTCGACATCATCGCCAGCAACCGCTCTCTTCAATCTACAC 185

Qy 63 CCAATCAGTCTCTCTACCCCGTCTGATCTCTCAATATCCGACTATGTCAGCAC 122

Db 186 CCAGATCAGTCTCGTTTACCCCGTCTGATCCCTCCAGTATCCCAACCATCGTCAGCAC 245

Qy 123 CTTTCGAGCAAGGCTTTAAGCGCTTCTCCGAAGCCCTCCCATGGTTCGACGGCCAGGTCAA 182
 Db 246 CTTTCGAGGAGGAGGCTTAAACGCTCTCTCAAACCTTCCCATGGTTCGCGGCCAGGTCAA 305
 Qy 183 ACCGAGGGGATAGGAGGGGAAACACAGGAATCTTCTTTATCGTCCCTTTTGAGGACGT 242
 Db 306 GACCCAGGGGATCAGCGAAGGAAACACAGGAATCTTCCAAAGATCATTTCCATATGAGGAGAC 365
 Qy 243 TCCTCGTGTGTAGTCAAGACCTCGCGATGATCTTTCAGCGCCACCATCGAGGTAT 302
 Db 366 ACCCGTCTTGTGGTGAAGAGCTTCGTGATGATCTTTCAGCGCCACCATCGAGGGTT 425
 Qy 303 GAGAAAGCGGGATACCTTATGCGGATGTTTTCAGGAGAACATCATCGCCCAAGGAGAC 362
 Db 426 GAGAAAGCGGGTTTCCCTCTAGAGATGTTTTCAGGAGAACGTCGTCGCTCCGAGGAAGAC 485
 Qy 363 GTTACTATTGACCTGGTACTGTCCTCCGACGA 395
 Db 486 ATTAGCTATCGGACCTGGCAATGGCCCAACGA 518

RESULT 12

Bi187780/c

LOCUS

DEFINITION

457 bp mRNA linear EST 10-JUL-2001

b2d04fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA sequence.

ACCESSION Bi187780

VERSION Bi187780.1 GI:14661459

KEYWORDS

SOURCE

ORGANISM

Fusarium sporotrichioides

Fusarium sporotrichioides

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

1 (bases 1 to 457)

Ren.Q., Tag.A., Peplow.A., Lai.H., Kupfer.C., Peterson.A., Beremand M. and Roe.B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished

Other ESTs: b2d04fs.r1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

655 5e-70 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: M13-20

High quality sequence stop: 257.

FEATURES

source

1. .457 Location/Qualifiers

/organism="Fusarium sporotrichioides"

/mol_type="mRNA"

/strain="Tri 10"

/db_xref="taxon:5514"

/clone="b2d04fs"

/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript

; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 109 a 128 c 104 g 116 t

ORIGIN

Query Match 19.8%; Score 268.4; DB 12; Length 457;
 Best Local Similarity 80.0%; Pred. No. 2.4e-65;
 Matches 328; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 947 ACTCGACCATCGCGAAATCGCAACAGTCACTCGCGCAACAGCATCAACGCTTCGTT 1006
Db |||||
QY 454 ACTCGACCGTCCCGGAATCGCAACGA-ACCTTGGCGCAACAGCATCACGCTCGCGT 396
Db |||||
QY 1007 CAGAACTGACCCCGGAGCATCGCCGACGCAACAGAGGTCTCGCGAGTACCTGCACA 1066
Db |||||
QY 395 CGAACTCAACAGTGAATCGTTTGGCAGACGCAACAGCTTTGGCGAGTACATCGCAT 336
QY 1067 ACAACCCCGACAGTCCCAACGATCCCTGACCGCTGATGCGGACCACTACCGAGTCA 1126
Db |||||
QY 335 GCCTCGCTGACAAGTCGAGCGTCTCCCTGACCGCGATCGGAATCCGTCAGACGATCA 276
QY 1127 TGCTGAGTCTTTGGCCCAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTA 1186
Db |||||
QY 275 TGCTGAGTCTCGGCGCAAGTGGGATGCTGGAGTATGACTTTGGGTTGGACTGGGTA 216
QY 1187 AGCCGAGACTGTGAGACGGCCAACTTTTGGACCTGTTGAGAGCTTGATGACTTTATGC 1246
Db |||||
QY 215 AGCCTGAGAGTGTGAGAAGACCTCGCTTTGAACCTTTTGAGAGTTTGATGACTTTATGC 156
QY 1247 CCAAGAAGCCTGATGCGGAGTCTGTGCGGCGCTTTCTGAGGATGAGGATATGGACC 1306
Db |||||
QY 155 CCAAGAAGCCTGATGCGGAGTGTACGGCGTCAATTTCTGAGGATGAGGATATGGAGA 96
QY 1307 GATTGAAGCGGATGAAGAGTGGACCAAGTATGCGCAGTACGTTGCTTAG 1356
Db |||||

RESULT 13
BI192452
LOCUS
DEFINITION
m4b09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone m4b09fs 5', mRNA
sequence.

ACCESSION
BI192452
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 392)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
Other ESTs: m4b09fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
557 3e-57 gi|437882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 361.

FEATURES
source
1..392
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="m4b09fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 98 a 121 c 92 g 81 t
ORIGIN
Query Match
Best Local Similarity 19.0%; Score 258; DB 12; Length 392;
Matches 316; Conservative 0; Mismatches 75; Indels 3; Gaps 1;
QY 347 TCGCCCAAGGAAGACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCCTG 406
Db |||||
QY 407 TAAATCTATTTCAGCTCAACTTCATCAAGGGCGGACTCATCTCTCACTGTCAACGACAGC 466
Db |||||
QY 61 TGTGCTATTGAGCTCAACTTCATTAAGGGCGGACTCATCTCACTCAACGACGACAC 120
QY 467 ACGGTGCTATGATGATGATGAGCCAAAGATGCGGTGATCCGCTACTCTCCAGGCGTGC 526
Db |||||
QY 121 ATGGTGTCTATGACATGACAGACCAAGATGAATATTTCGCTCTCTCCAAGGCGTGC 180
QY 527 GTAACGACCCATTCAACGAGAGGAATGAGGCCATGAACCTCGATCGCAAGACGATAG 586
Db |||||
QY 181 CCAACGAATATTTCACCGAGGAGGAATCTCGGCCATGAACCTCGATCGAAGACGCTAG 240
QY 587 TTCCTTACCTTGAACACTATACGATGSCCCGAGGTAGATCATCAGATTGTCAAGCTG 646
Db |||||
QY 241 TCCCTCTCCTTGAACACTTACAAAGTTGCTCTGAGCTATACCAAGATCGCCAAAC 298
QY 647 ATGTAGCTGGTGGTGACGCTCTCTCACGCCGCTCAGTGCAGCTGGGCGCTTCTTCACAT 706
Db |||||
QY 299 -TGGCCTGTGGCGAGCTCCACCCGACCGCCCAAGGCTGGGCGTCTTTTCAT 357
QY 707 TCAGCCCCAAGGCCATGTCAAGCTCAAGGATGC 740
Db |||||

RESULT 14
BI192498/c

LOCUS
DEFINITION
m4f10fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone m4f10fs 3', mRNA
sequence.

ACCESSION
BI192498
VERSION
KEYWORDS
SOURCE
ORGANISM
Fusarium sporotrichioides
Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 423)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
Other ESTs: m4f10fs.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
652 3e-68 gi|437882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 290.

FEATURES
source
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Location/Qualifiers
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"

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/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 105 a 121 c 92 g 105 t
ORIGIN
Query Match 18.8%; Score 254.8; DB 12; Length 423;
Best Local Similarity 79.6%; Pred. No. 1.7e-61;
Matches 301; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 979 CTCGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGA 1038
Db 423 CTTGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGA 364
QY 1039 ACAGAGGCTTCGCGAGCTACCTGCGACAAACCCCGACAGTCCCAAGCTATCCCTGACG 1098
Db 363 ACAAGAGCTTCGCGAGCTACCTGCGACAAACCCCGACAGTCCCAAGCTATCCCTGACG 304
QY 1099 GCTGATGCGGACCATCTACACAGCTCATGCTGAGTTCTTGGGCCAAGGTGGGACTCTGG 1158
Db 303 GCGGATGCGGATCCGTCAGCAGCATCATGCTGAGTTCTTGGGCCAAGGTGGGACTCTGG 244
QY 1159 GATTAGGACTTTGGGCTCGGACTTGGGTAAGCCGAGACTGTGAGAGCGGCAATCTTTGAG 1218
Db 243 GAGTATGACTTTGGGTTTGGACTGGGTAAGCCCTGAGAGTGTGAGAGACTCTCGCTTGAC 184
QY 1219 CTTGTTGAGAGCTTGATGATCTTTATGCCCAAGAGCTGATGCGGAGTTCTGTGGGCG 1278
Db 183 CCTTTTGGAGTTTGATGATCTTTATGCCCAAGAGCTGATGCGGAGTTCTGTGGGCG 124
QY 1279 CTTTCTGAGGATGAGGATATGACCGGATTAAGCGCGGATAGGAGTGGACCAAGTAT 1338
Db 123 ATTCTCTGAGGATGAGGATATGAGAGACTTAAGCGCGGATAGGAGTGGACCAAGTAT 64
QY 1339 GCGCAGTACGTTGGTTAG 1356
Db 63 GCAAGTATATGGGTAG 46
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High quality sequence stop: 443.
Location/Qualifiers
1. 490
/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 129 a 153 c 104 g 103 t
ORIGIN
Query Match 18.5%; Score 251.2; DB 12; Length 490;
Best Local Similarity 81.1%; Pred. No. 2e-60; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 68;
QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTTACCAGGCTCTCTTTTCGATCTACAC 62
Db 129 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTTCTTTCAATCTACAC 188
QY 63 CCAATACAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTCTCAGCAC 122
Db 189 CCAGATCAGTCTCGTTTACCCCGTCTCTGATTCCTCCAGTATCCCACTATTCGTCAGCAC 248
QY 123 CTTGAGCAAGGCTTAAAGCGCTTCTCGAAGCGCTCCCATGGTGGCAGGCCAGGTCAA 182
Db 249 CCTTGAGGAAGGCTTAAAGCGCTCTCTCAAACTTCCCATGGTCCGGCCAGGTCAA 308
QY 183 AGCGAGGCGCATTAAGCGAGGGAACACAGGAACCTCTCTTATCTCTCTTTTGAGGACGT 242
Db 309 GACCGAGGCGATCAGCGAAGGAACACAGGAACCTTCCAGATCATTCATATGAGGAGAC 368
QY 243 TCCTCGTGTGTAGTGAAGACCTTCGCGATGATTCCTTACGCGCCACGATCGAGGATAT 302
Db 369 ACCCGCTTGTGTGAGGAAGACCTTCGCGATGATTCCTCAGCGCCAAAGATCGAGGGGTT 428
QY 303 GAGAAAGCGGATACCCCTATGGCGATGTTTGAGGAGAACATCATCGCCCAAGGAAGAC 362
Db 429 GAGAAAGCGGCGGTTTCCCTTAGAGATGTTTGAGGAGAACATCATCGCTCGCGAGGAGAC 488

Search completed: February 7, 2004, 21:46:40
Job time : 3192 secs

RESULT 15
BI201353 490 bp mRNA linear EST 10-JUL-2001
LOCUS p2e12fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone p2e12fs 5', mRNA
sequence.
ACCESSION BI201353
VERSION BI201353.1 GI:14667325
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE 1 (bases 1 to 490)
AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
M., and Roe, B.
TITLE Analysis of a Fusarium sporotrichioides EST database
JOURNAL Unpublished
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
656 1e-68 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 21:46:44 ; Search time 530 Seconds

(without alignments)
9424.540 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacacgct.....atgcgcagtaogttggttag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 48999406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:**

- 1: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubnpa/PCTUS_PUBCOMB.seq*
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- 9: /cgn2_6/ptodata/1/pubnpa/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubnpa/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubnpa/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubnpa/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubnpa/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubnpa/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubnpa/US10C_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq*
- 17: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq*
- 18: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	14	US-10-074-279-5
2	915.6	67.5	1403	14	US-10-074-279-1
3	915.6	67.5	12949	14	US-10-074-279-11
4	915.6	67.5	13737	14	US-10-074-279-10
5	249.8	18.4	1425	14	US-10-074-279-7
C 6	39.2	2.9	1947	12	US-10-369-493-27681
C 7	35.8	2.6	2463	12	US-10-320-797-7
8	35.4	2.6	2400	12	US-10-369-493-37751
C 9	35.2	2.6	837	15	US-10-184-644-352
C 10	35.2	2.6	837	15	US-10-184-634-352
C 11	35	2.6	556	13	US-10-063-685-24
C 12	35	2.6	556	15	US-10-184-644-136
C 13	35	2.6	556	15	US-10-184-634-136
14	34.6	2.6	427	12	US-10-374-780A-932
15	34.6	2.6	1112	13	US-10-027-632-31187

16	34.6	2.6	1112	13	US-10-027-632-31188
17	34.6	2.6	1112	14	US-10-027-632-31187
18	34.6	2.6	1112	14	US-10-027-632-31188
C 19	34.2	2.5	1377	12	US-10-369-493-46533
20	33.8	2.5	322	12	US-10-242-535A-19650
21	33.8	2.5	2955	10	US-09-880-107-2148
22	33.8	2.5	2955	11	US-09-918-624B-30
23	33.8	2.5	2994	15	US-10-084-817-92
24	33.8	2.5	3075	13	US-10-240-965-135
C 25	33.6	2.5	594	13	US-10-140-472-10
C 26	33.6	2.5	594	13	US-10-141-761-10
C 27	33.6	2.5	594	13	US-10-142-885-10
C 28	33.6	2.5	594	13	US-10-158-790-10
C 29	33.6	2.5	594	13	US-10-137-871-10
C 30	33.6	2.5	594	13	US-10-140-805-10
C 31	33.6	2.5	594	13	US-10-140-864-10
C 32	33.6	2.5	594	13	US-10-140-923-10
C 33	33.6	2.5	594	13	US-10-141-756-10
C 34	33.6	2.5	594	13	US-10-141-759-10
C 35	33.6	2.5	594	15	US-10-123-155-10
C 36	33.6	2.5	594	16	US-10-146-731-10
C 37	33.6	2.5	625	13	US-10-140-472-70
C 38	33.6	2.5	625	13	US-10-141-761-70
C 39	33.6	2.5	625	13	US-10-142-885-70
C 40	33.6	2.5	625	13	US-10-158-790-70
C 41	33.6	2.5	625	13	US-10-137-871-70
C 42	33.6	2.5	625	13	US-10-140-805-70
C 43	33.6	2.5	625	13	US-10-140-864-70
C 44	33.6	2.5	625	13	US-10-140-923-70
C 45	33.6	2.5	625	13	US-10-141-756-70

ALIGNMENTS

RESULT 1
US-10-074-279-5
; Sequence 5, Application US/10074279
; Publication No. US2002062136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-10-074-279-5

Query Match 100.0%; Score 1356; DB 14; Length 1356;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTTCAAGATACAGCTCGACCTCGGCAGCTACCGGCTCTTTGATCTAC 60
Db 1 ATGGCTTCAAGATACAGCTCGACCTCGGCAGCTACCGGCTCTTTGATCTAC 60
QY 61 ACCCAATCAGTCTCTCTTACCCGCTCTGATCTCTCAATATCCCATTTGTCAGC 120
Db 61 ACCCAATCAGTCTCTCTTACCCGCTCTGATCTCTCAATATCCCATTTGTCAGC 120

QY 121 ACCTTCGAGCAGGCTTTAAGCGCTTCTCCGAGCGCTCCCATGGTTCGACGCCAGGTC 180
Db 121 ACCTTCGAGCAGGCTTTAAGCGCTTCTCCGAGCGCTCCCATGGTTCGACGCCAGGTC 180
QY 181 AAGCGCGAGGCGATTAGCGAGGGAACACAGGAACTTCTCTTATCGTCCCTTTTGGAGGAC 240
Db 181 AAGCGCGAGGCGATTAGCGAGGGAACACAGGAACTTCTCTTATCGTCCCTTTTGGAGGAC 240
QY 241 GTTCTCTGTTGTAGTGAAGAACCTTCGCGATGATCTTCAAGCGGCCACGATCGAGGGT 300
Db 241 GTTCTCTGTTGTAGTGAAGAACCTTCGCGATGATCTTCAAGCGGCCACGATCGAGGGT 300
QY 301 ATGAGAAAGCGCGGATACCTATGGCGATGTTTGAAGAAATCATATCGCGCCAAAGAAAG 360
Db 301 ATGAGAAAGCGCGGATACCTATGGCGATGTTTGAAGAAATCATATCGCGCCAAAGAAAG 360
QY 361 AGTTTACCTATTGGACCTGCTACTGCTCCGACGACCCAAAGCCTCTTAATTTCTATTCGAG 420
Db 361 AGTTTACCTATTGGACCTGCTACTGCTCCGACGACCCAAAGCCTCTTAATTTCTATTCGAG 420
QY 421 CTCAACTTCATCAAGGCGGAGCTCATCTCACTGTCACGAGCAGCAGCGTGTCTATGGAT 480
Db 421 CTCAACTTCATCAAGGCGGAGCTCATCTCACTGTCACGAGCAGCAGCGTGTCTATGGAT 480
QY 481 ATGGTAGGCCAAGATGCGGTGATCCGCTACTCTCAAGCGCGGCGGTAAAGCCCATTC 540
Db 481 ATGGTAGGCCAAGATGCGGTGATCCGCTACTCTCAAGCGCGGCGGTAAAGCCCATTC 540
QY 541 ACCGAGAGGAAATGACGGGCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600
Db 541 ACCGAGAGGAAATGACGGGCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600
QY 601 AACTATACGATTGGCCCCGAGGTAGATCATCAGATGTTCAAGTGATGATGCTGGTGGT 660
Db 601 AACTATACGATTGGCCCCGAGGTAGATCATCAGATGTTCAAGTGATGATGCTGGTGGT 660
QY 661 GAGCTGTTCTCAGCGCGTCAGTGCAAGCTGGCGGTTCTTCACTTCACTCAGCCCAAGGCC 720
Db 661 GAGCTGTTCTCAGCGCGTCAGTGCAAGCTGGCGGTTCTTCACTTCACTCAGCCCAAGGCC 720
QY 721 ATGTGAGAGCTCAAGGATGCTGTCTACCAAGACTTTCGACGATCAACAAAGTTCTGTCTG 780
Db 721 ATGTGAGAGCTCAAGGATGCTGTCTACCAAGACTTTCGACGATCAACAAAGTTCTGTCTG 780
QY 781 ACTGACGATGCTCTTTCGCGGTTCACTGGAATCGGCTCTCGCGTCTCGGCAAGA 840
Db 781 ACTGACGATGCTCTTTCGCGGTTCACTGGAATCGGCTCTCGCGTCTCGGCAAGA 840
QY 841 ATCGATGGCTCTGACCTACCGAGTCTGCGGTCTGTGATGCTCGACCGGCAATGGGT 900
Db 841 ATCGATGGCTCTGACCTACCGAGTCTGCGGTCTGTGATGCTCGACCGGCAATGGGT 900
QY 901 GTCTCGAACAACTACCCAGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 960
Db 901 GTCTCGAACAACTACCCAGGCTTCTTCAAAACATGACCTACCAACATCGACCATCGGC 960
QY 961 GAAATCGCCACAGATCACTGCGGCGAAACAGCATCAAGCTGCTGTTGAACTCGACCCC 1020
Db 961 GAAATCGCCACAGATCACTGCGGCGAAACAGCATCAAGCTGCTGTTGAACTCGACCCC 1020
QY 1021 GCGAGCATGCGCCAGCAAGAGGTTCTCGGAGTACCTGCAACAAACCCGCAAG 1080
Db 1021 GCGAGCATGCGCCAGCAAGAGGTTCTCGGAGTACCTGCAACAAACCCGCAAG 1080
QY 1081 TCCAACTGATCCCTGACCGCTGATGCGGACCCATCTACCGCTCATCTGAGTCTTTGG 1140
Db 1081 TCCAACTGATCCCTGACCGCTGATGCGGACCCATCTACCGCTCATCTGAGTCTTTGG 1140
QY 1141 GCCAAGGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTAAGCCCGGACTGTG 1200
Db 1141 GCCAAGGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTAAGCCCGGACTGTG 1200
QY 1201 AGACGGCCAACTTTGAGCCTGTTGAGAGCTTTGATGATCTTTATGCCCAAGAGCCTGAT 1260

Db 1201 AGACGGCCAACTTTGAGCCTGTTGAGAGCTTTGATGATCTTTATGCCCAAGAGCCTGAT 1260
QY 1261 GCGGAGTCTGTCGCGCGCTTCTCTGAGGATGAGGATGACCGGATTTGAAGGCGGAT 1320
Db 1261 GCGGAGTCTTCTGTCGCGCGCTTCTCTGAGGATGAGGATGACCGGATTTGAAGGCGGAT 1320
QY 1321 AAGGAGTGGACCAAGATGATGCGAGTACGTTGGTTAG 1356
Db 1321 AAGGAGTGGACCAAGATGATGCGAGTACGTTGGTTAG 1356

RESULT 2
US-10-074-279-1
; Sequence 1, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-1

Query Match 67.5%; Score 915.6; DB 14; Length 1403;
Best Local Similarity 80.3%; Pred. No. 1.4e-306;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGCGCAGCTACAGGCTCTCTTCGATCTACAC 62
Db 36 GTCTTTTGATAGAGCTCGACATCATCGCGCCAGCAACCGCTCTTCTTCAATCTACAC 95
QY 63 CCAATCAGTCTCTCTACCCGCTCTCTGATCTCTCAATATCCCACTATTGTGAGCAC 122
Db 96 CCAGATCAGTCTCTGTTTACCCCGCTCTGATCTCTCCAGTATCCCACTATCGTCAGCAC 155
QY 123 CTTGAGCAAGGCTTAAAGCGCTTCTCCGAGCGCTCCCATGGGTGCGAGCCAGGTCAA 182
Db 156 CTTGAGCAAGGCTTAAAGCGCTTCTCTCAAACTCTCCCATGGGTGCGAGCCAGGTCAA 215
QY 183 AGCCGAGGCGATTAGCGAGGAAACACAGGAACTTCTCTTATCGTCCCTTTTGGAGCAGT 242
Db 216 GAACGAGGCGATTAGCGAGGAAACACAGGAACTTCTCAAGATCATTCATATGAGGAGAC 275
QY 243 TCCTGCTGTTGATGAGAAAGCTTCGCGATGATCTTCAGCGCCCGCATCGAGGGTAT 302
Db 276 ACCCGCTGTTGTTGAGAAAGCTTCGCGATGATCTTCAGCGCCCGCATCGAGGGT 335
QY 303 GAGAAAGCGGATACCTATGCGGATGTTTGAAGAGAAATCATTCGCGCCCAAGGAAGAC 362
Db 336 GAGAAAGCGGATTCCTCTTAGAGATGTTTGAAGAGAACTTCGCTCGCTCCGAGGAGAC 395
QY 363 GTTACCTATTGCACTGCTGATGCTGCGAGCAACCAAGCTGTATTTCTATTGACGT 422
Db 396 ATTAGCTATCGGACTGCGCAATGGCCCAAGCAACCGGAAAGCTGTGTTGCTATTGACGT 455
QY 423 CAATCTATCAAGGGCGGACTCATCTCCTCAACGAGCAGCAGCGTGTCTATGATAT 482
Db 456 CAACTTCAATGAGCGGCGGACTCATCTCCTCAACGAGCAACATGTTGCTATGAGCAT 515

483 GGTAGCCCAAGATGGGTGATCGCTACTCTCCAGGCGTCCGTACAGCCCAATTCAC 542
516 GACAGGCAAGATGCAATATTTGCTCTTCTCCAGGCGTCCGCAAGCAATCAATTCAC 575
543 CGAAGAGAAATGACGGCCATGAACCTCGATCGGCAAGACGATAGTTCTTACCTTGA AAA 602
576 CGAGGAGAAATCTCGGCCATGAACCTCGATCGGCAAGACGATAGTTCTTCTTGA AAA 635
603 CTATACGATTTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTGTTGTTGA 662
636 CTACAAAGTTGGTCTGAGCTAGACCAACAGATGCCAAACCC---TGCGCCTGTGGCGA 692
663 CGCTGTTCTACGGCGGTGAGTGAAGCTGGCGGTTCTTCAATTCACAGCCCAAGGCCAT 722
693 CGCTCCACCCGACCGGCAAGGCAAGCTGGCGGTTCTTCAATTCACAGCCCAAGGCCAT 752
723 GTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCAATCAACAAAGTTTGGTGCAC 782
753 CTCGAGCTGAAGACGAGCCAGCAACAAAGACTCTTGACGCGTGTCCAAGTTTGTCAAC 812
783 TGACGATGCTCTTCGGCGTTTCACTTGGAATTCGGCCCTCTCGCGTGTCTCGAAAGAA 842
813 TGATGATGCTCTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTACGCTCGCAAGATT 872
843 CGATGGCTCTGACCTACCGAGTTCTGCGGTGCTGTGATGCTCGACCGGCAATGGTGT 902
873 GGATGCTTCCACACTACTGAATTTCTGCGCGGTGTGACATGCGGGGCCCAATGGCGGT 932
903 CTCGAAACAATPACCGAGGCTTTCTCAAAATGATGACCTTACCACAACTCGACCATCGGCGA 962
933 ATCAAGCACATACCGAGGCTTTCTCAAAATGATGACCTTACATGACCTCGACCGTGGCGA 992
963 AATCGCAACGAGTCACTCGGCGCAACAGCAATCAAGCTTCTGTTTCAAGAACTCGAACCGC 1022
993 AATCGCAACGAAACCACTTGGCGCAACAGCAATCAAGCTTCTGTTTCAAGAACTCGAACCGC 1052
1023 GAGCATGGCCAGGCAACAGAGTCTCGGAGTCTCGGAGTCTGATGCTCGACCGGCAAGTGC 1082
1053 TCGTTTGGCGAGAGCAACAAAGCTTTGGCGACGTACATGATGCGCTGCGCTGCAAGTC 1112
1083 CAACGATATCCCTGACGCTGATGGGACCACTTACACAGCTCATGCTGAGTTCTTGGCG 1142
1113 GAGGCTCTCTGACCGCGGATGGAATCGTCAAGCAATCATGCTGAGTTCTTGGCG 1172
1143 CAAGTGGAATCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG 1202
1173 CAAGTGGAATCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG 1232
1203 ACGGCCAATCTTGGGCTGTTGAGCTTGTGAGTCTGATGCTTTATGCGGCAAGGCTGTAG 1262
1233 AAGACCTCGCTTTGAACTTTTGGAGGTTTGTATGATGCTTTATGCGGCAAGGCTGTAG 1292
1263 CGAGTTCTGTCGGCGCTTTCTCTGAGGATGAGATGATGACCGATTGAGGCGGATAA 1322
1293 GGAGTTTACGGCTGCAATTTCTGAGGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1352
1323 GGAGTGACCAAGTATCGGAGTACGTTGGTTAG 1356
1353 GGAGTGACCAAGTACGCAAGTATATTTGGGTAG 1386

RESULT 3

US-10-074-279-11
; Sequence 11, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Query Match 67.5%; Score 915.6; DB 14; Length 12949;

Best Local Similarity 80.3%; Pred. No. 4.7e-306;

Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY	3	GGCTTTCAGATACAGCTCGACACCCCTCGGCGAGCTACCGAGCCCTCTTTTCGATCTACAC	62
Db	11281	GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTTCTTCAATCTACAC	11340
QY	63	CCAAATCAGTCTCTCTACCCGCTCTGTCTCAATCTCAATCCCACTATTGTTCAGCAC	122
Db	11341	CCAGTACGTCCTGTTTACCCGCTCTGTATCCCTCCAGTATCCCACTCGTCAGCAC	11400
QY	123	CTTCGAGCAAGCTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTGCGAGGCCAGGTCAA	182
Db	11401	CTTTGAGGAGGCTTAAACCGCTCTCTCAAACTTCCCATGGGTGCGGCCAGGTCAA	11460
QY	183	AGCCGAGGCAATAGCGAGGGAACACAGGAACCTTCTTTATCGTCCCTTTTGAGGACGT	242
Db	11461	GACCGAGGCAATAGCGAGGGAACACAGGAACCTTCCAAAGATCATTCATATGAGGAGAC	11520
QY	243	TCCTGCTGTTGATGAAAGACCTCCGCGATGATCTTCAGCGCCAGCATCGAGGATAT	302
Db	11521	ACCCGCTGTTTGTGTGAAAGACCTCCGCGATGATCTTCAGCGCCAGCATCGAGGATAT	11580
QY	303	GAGAAAGCGGGATACCTATGCGGATGTTTACGAGAAATCATTCGCGCCAGGAGAC	362
Db	11581	GAGAAAGCGGGATACCTATGCGGATGTTTACGAGAAATCATTCGCGCCAGGAGAC	11640
QY	363	GTTACCTATTGGAACCTGGTACTGTCGCGACGACCCAAAGCCTGTAATTTTCAGCT	422
Db	11641	ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCTGTGTTGCTATTTCAGCT	11700
QY	423	CAACTTCATCAAGGCGGACCTCATCTCAGTGTCAACGAGCAGCACGCTGTATGATAT	482
Db	11701	CAACTTCATTAAGGCGGACCTCATCTCAGTGTCAACGAGCAGCACGCTGTATGATAT	11760
QY	483	GGTAGGCAAGATCGGCTGATCGCTACTCTCCAAAGCGTCCGTAACGACCCATTCAC	542
Db	11761	GACAGGCAAGATGCAATTAATTCGCTCTCTCCAAAGCGTCCGTAACGACCCATTCAC	11820
QY	543	CGAAGAGAAATGACGGCCATGAACTTCGATTCGCAAGACGATAGTTCTTACCTTGA AAA	602
Db	11821	CGAAGAGAAATCTCGGCCATGAACTTCGATTCGCAAGACGATAGTTCTTACCTTGA AAA	11880
QY	603	CTATACGATTTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTGTTGTTGA 662	
Db	11881	CTACAAAGTTGGTCTTGAGCTAGACCAACGATGCGCAAAACCC---TGCGCTGTGCGCA 11937	
QY	663	CGCTGTTCTCACGCGGTGAGTCAAGCTGGGCTTCTTCAATTCAGCCCAAGGCCAT 722	
Db	11938	CGCTCCACCCGACCGGCAAGGCAAGCTGGGCTTCTTCAATTCAGCTCCCAAGGCCCT 11997	
QY	723	GTCAAGCTCAAGATGCTGCTACCAAGACTTTGACGCACTCAACAAAGTTTGGTTCGAC 782	
Db	11998	CTCGAGCTCAAGAGCGCAGCCCAAGACTTTGACGCGTCTGTCAGTTTGTGTCAAC 12057	
QY	783	TGAGATGCTCTTTCGGCGTTTCACTTGGAAATCGGCTCTCGCGTGTGCGTCTCGAAGAA 842	

Db	12058	TGATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGCTACGTTCTGCAAGATT	12117
Qy	843	CGATGGCTCTGCACCTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGGCAATGGGTGT	902
Db	12118	GGATGCTTCCACACCTACTGAAATCTGCGGCTGTGACATGCGGGGCCCAATGGGCGT	12177
Qy	903	CTCGAACAACCTACCGAGCCTTTCTCAAAACATGACCTACCAACATCGACCAATCGGCGA	962
Db	12178	ATCAAGCACATACCCAGGCTTTCTCAAAACATGACCTACCAACATCGGCGGCGA	12237
Qy	963	AATCGCAACGAGTCACTCGGCGCAACAGAGTCTCGCGAGCTACCTGACAAACCCCGCAAGTC	1022
Db	12238	AATCGCAACGAGTCACTCGGCGCAACAGAGTCTCGCGAGCTACCTGACAAACCCCGCAAGTC	12297
Qy	1023	GAGCATGCGCGAGCAACAGAGTCTCGCGAGCTACCTGACAAACCCCGCAAGTC	1082
Db	12298	TCGTTTGGCGAGACCAACAGCTTTGGCGAGCTATGATGATGCGCTGCTGACAGTC	12357
Qy	1083	CAAGTATCCCTGACGGCTGATGGGACCCCACTTACCAGCGTCACTGCTGAGTCTTGGGC	1142
Db	12358	GAGCTCTCCCTGACCGCGATGCAATCCCTGACAGCATCATGCTGAGTCTTGGGC	12417
Qy	1143	CAAGTGGGACTCTGGGATACAGCTTTGGGCTCGGACTGGTGAAGCCCGAGCTGTGAG	1202
Db	12418	CAAGTGGGATGCTGGGAGTATGACTTTGGGCTTTGGACTGGGTAAGCCTGAGTGTGAG	12477
Qy	1203	ACGCCAATCTTTCAGCTGTTGAGAGCTTTCATGTTATGCCCCAAGAGCCTGATGG	1262
Db	12478	AAGACCTCGCTTTGAACCTTTTGAAGTGTGATGTTATGCCCCAAGAGCCTGATGG	12537
Qy	1263	CGAGTTCTGTGCGGCGCTTCTCTGAGGGAATGAGGATGAGCGATTTGAAGCGGATAA	1322
Db	12538	GGAGTTTACGGGCTCCATTTCTCTGAGGATGAGGATGAGGACTTAAGCGGATGA	12597
Qy	1323	GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG	1356
Db	12598	GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG	12631
RESULT 4			
US-10-074-279-10			
; Sequence 10, Application US/10074279			
; Publication No. US20020162136A1			
; GENERAL INFORMATION:			
; APPLICANT: Hohn, T.			
; APPLICANT: Salmeron, J.			
; APPLICANT: Peters, C.			
; APPLICANT: Kendra, D.			
; APPLICANT: Reinders, J.			
; APPLICANT: Kuznia, R.			
; APPLICANT: Dill-Mackey, R.			
; TITLE OF INVENTION: Transgenic Plant and Methods			
; FILE REFERENCE: sequencelist			
; CURRENT APPLICATION NUMBER: US/10/074,279			
; CURRENT FILING DATE: 2002-02-12			
; PRIOR APPLICATION NUMBER: US/09/538,414			
; PRIOR FILING DATE: 2000-03-29			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 10			
; LENGTH: 13737			
; TYPE: DNA			
; ORGANISM: Plasmid			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid			
US-10-074-279-10			
Query Match 67.5%; Score 915.6; DB 14; Length 13737;			
Best Local Similarity 80.3%; Pred. No. 4.9e-306;			
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;			
Qy	3	GGCTTTCAAGATACAGCTCGACACCTCGGCGGAGTACAGGCGCTCTTTCGATCTACAC	62

QY 1143 CAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGACTGGGTAGCCCGAGCTGTGAG 1202
|||||
DB 1187 CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAAGCCTGAGAGTGTGAG 1246
|||||
QY 1203 ACGGCCAATCTTTGAGCCCTGTTGAGAGCTTGTGATGTAATTTATGCCCAAGAGCCCTGATGG 1262
|||||
DB 1247 AAGACCTCGCTTTGAACCTTTGAGAGTTGATGTAATTTATGCCCAAGAGCCCTGATGG 1306
|||||
QY 1263 CGAGTTCTGTGGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTAAGAGCGGATAA 1322
|||||
DB 1307 GGAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGGCGGATGA 1366
|||||
QY 1323 GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356
|||||
DB 1367 GGAGTGGACAAAGTACGCAAGTATATTGGGTAG 1400
|||||

RESULT 5
US-10-074-279-7
; Sequence 7, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-7

Query Match 18.4%; Score 249.8; DB 14; Length 1425;
Best Local Similarity 51.9%; Pred. No. 2.4e-75;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGCTCGACACCCCTCGGCCAGCTACCGGCTCTCTTCGATCTACACCAATCAGTCTC 75
DB 64 CAATTTGATATTTGGGACAAACCTTCGCTATACAACTATACACTCAATAATGCTCT 123
QY 76 CTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTGTGAGCACTTCGAGCAAGGT 135
DB 124 ATCTACCGTGTAACAGATCTCTCTCATGACCATATCTGTAATACCTTAAACAGGA 183
QY 136 CTTAAGCGCTTCTCGAAGCGTCCATGGTTCGAGCGCCAGGTCAAGCCGAGGCAT 195
DB 184 CTTGAAACATTTGGCTTAAATTTCCAGTGGCTAGCAGGAAATGCTGTAATGAAAGTCT 243
QY 196 AGCGAGGGAACACAGGAATCTCTTTATCTCTCTTTGAGGAGCTTCCTCGTTGTA 255
DB 244 GACGAGGTAACTGGTACCTTACGAATTTGCCGTGAGCAAAATTTCCAC---TTATC 300
QY 256 GTGAAAGACCTCCGCGATGATCTCTTCAGCGCCACGATCGAGGGTATGAGAAAGCGGGA 315
DB 301 GTCCAAGATCTTCGAGAGATCTGTCTGCCCCAACATATGATTCGCTTGAAGAGCTGAC 360
QY 316 TACCTATGGGATGTTTGAAGAGAACATATCGCGCAAGGAAGACGTT-----ACCT 369
DB 361 TTTCTATCTACATGTTAGAGCAAAAGACTTTTGGGCTTTCATGACTATCAATCCACCT 420
QY 370 ATTGGACCTGTACTGTGTCCTCGACGACCAAGCCTGTAATCTTATTTCAGCTCAATTC 429

RESULT 6

US-10-369-493-27681/c

; Sequence 27681, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

DB 421 GGAACATATAGTATGGCCGCCAAGAGTGGGCTCTGATTTGCAAGTCAAGCAAACTTT 480
|||||
QY 430 ATCAAGGGCGGACTCATCTCTCAACGACGACGAGCTGCTATGATATGTTAGGC 489
|||||
DB 481 ATCTCCGGCGGCTCTGCTTAACATTTCTCGGGCAGCACATATTATGATATACAGGA 540
|||||
QY 490 CAAGATGCGGTGATCCGTCCTACTCTCAAGGGGTGCGGTAAAGCCATTCACCGAAGAG 549
|||||
DB 541 CAGGAAAGTATCATCAACTTGTCTCAATAAATCTTGCCACCAAAAACCTTTCTCTGATGA 600
|||||
QY 550 GAATATGACGGCCATCAACCTCGATCGCAGAGCAGTAGTTCTCTTACCTTGGAAACTATAG 609
|||||
DB 601 GAATGCTCATTTGGAATATATAGATAAAAGCAAACTATTCTCTTTGTTGATGAACACTTGG 660
|||||
QY 610 ATT---GGCCCCGAGGTAGATCATCAATTTGCAAAAGCTGATAGCTGGGTGACCGCT 666
|||||
DB 661 GAAACCGACACACGCTAGTTTCATGAATAGTGGAACTCTAGAAATACAAGTGGAGAG 720
|||||
QY 667 GTTCTCAGCCGCTCAGT-----GCAAGCTGGGCGGTTCTTCAATTCAGCCCCAAG 717
|||||
DB 721 GAAAAGGAAACAGTCTTGTCTTCGAACTCTACTTTGGGCTTATGTTGAATTTTCTGCTATC 780
|||||
QY 718 GCCATGTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTCAGCGATCAACAAGTCTGTG 777
|||||
DB 781 TCATTGCAAGATCTGAGGATTTTGGCAATGCAGACATGATCTTCTGGCACAAAATTTGTC 840
|||||
QY 778 TCGACTGACGATGCTCTTTTCGGCGTTTCATCTGGAATACGGGCTCTCGCGTGGCTCGAA 837
|||||
DB 841 TCCACTGATGATATCGTACCTGCTTTTCATCTGGAATACAGTTTCTCGAGCCGTTTATCT 900
|||||
QY 838 AGAATCGATGCTCTGACCTTACCGAGTTCTGCGGTGCTGTGTGATGCTCGACCGGCAATG 897
|||||
DB 901 CGACTTAAACCAAGAAACGAAATCAAATTTAGGGCGTGTGTGGATGTTAGAAAACGGCTA 960
|||||
QY 898 GGTGCTCGAAACACTACCGAGGCTCTTTCAAACATGACCTTACCACAACTCGACCATC 957
|||||
DB 961 GGACTCCCCGAAACGATATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020
|||||
QY 958 GCGAAATCGCCAAACGAGTCACTCGGCGCAACAGCATCACGCTTCGTTTCAGAACTCGAC 1017
|||||
DB 1021 ABAAGCTTGGATCATATAAAGTTTGGGCGTTCTTGATCAGATTCGCAAGAGTAGAC 1080
|||||
QY 1018 CCCGCGAGCA-----TGCGCCAGCGAACAGAGGTCTCGCGACGTACTCTGCACAAAC 1071
|||||
DB 1081 CCTAAAGCTTTCGATTTGGCCCTATAATACATGCGCACTTGCTACGCTCTTAGCCGATGC 1140
|||||
QY 1072 CCCGACAGTCCAAAGTATCCCTGACGGCTGATGGGACCCATCTACAGGCTCATGCTG 1131
|||||
DB 1141 CCGGACAGACTAAGGTTTCTATACCTCAACCAATGATACTTTTATCTGSAATTTATGGTC 1200
|||||
QY 1132 AGTTCTTTGGGCAAGGTGGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGGTAAGGCC 1191
|||||
DB 1201 AGTTCTGTTGGCAAAAGTCAGCTCTATGACGTTGATTTCAATCTAGGGCTTGGAGAGGCC 1260
|||||
QY 1192 GAGACTGTGAGACGGCAAACTTTGAGCTGTTGAGAGCTTGTATGATCTTTATGCCCAAG 1251
|||||
DB 1261 AAGAGTGTATCGACGCGCGCTTCATTTCCCTTGAGAGCCCTAAATATATTTTATGCTAGA 1320
|||||
QY 1252 AAGCTGATGCGAGTCTGTGCGCGGCTTCTCTGAGGATGAGGATATGACCGGATG 1311
|||||
DB 1321 TCCTCCAGAGGTGAAATGGTGGTTGCTCTTTGCTTTAGAGATAAAGATTTGGAGTGCCTG 1380
|||||
QY 1312 AAGCGGATAAGGAGTGGACCAAGTATGC 1340
|||||
DB 1381 AATCGGATAAGAGATGACAAATTTATGC 1409
|||||

; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10 (52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 27681
 ; LENGTH: 1947
 ; TYPE: DNA
 ; ORGANISM: Neurospora crassa
 ; US-10-369-493-27681

	Query Match	2.9%	Score 39.2;	DB 12;	Length 1947;
	Best Local Similarity 53.2%;				
	Matches 83; Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;	
QY	1050	CGCGAGTACCTGCACAAACCCGCAAGTCCACGTATCCCTGACGGCTGATGGGA	1109		
Db	1854	CCCGACATAGCTGTGCGACACCAAGTCATGACAAACGTGAATGGCCGCGCTGTGGCGG	1795		
QY	1110	CCCATCTACACAGCGTATGCTGAGTCTCTGGCGCAAGGTGGGATCTGGGATACCACTT	1169		
Db	1794	CGCTGGAACTGGCCCTTCATGTTTCATGCGGGAAGCTGGCGCTCTTGGCGCCGATC	1735		
QY	1170	TGGGCTCGGACTGGGTAAAGCCGAGACTGTGAGACG	1205		
b	1734	GTAATGGGCTGTCAAAAGTGAACAAAGGTGAAGG	1699		

```

RESULT 7
US-10-320-797-7/c
; Sequence 7, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zarudko, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320.797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
; US-10-320-797-7

```

	Query Match	2.6%;	Score 35.8;	DB 12;	Length 2463;
	Best Local Similarity	53.1%;	Pred. No. 0.66;		
	Matches	76;	Conservative 0;	Mismatches 67;	Indels 0; Gaps 0;
Qy	2	TGGCTTTCAAGATACAGCTGCACACCCCTCGGCCAGCTACACAGGCCTCTCTTCGATCTACA	61		
Db	2371	TGGGTTTCAACAACTGGGTCGTGAGCTCGCCAAAGCAAGAAAAGAACTCGGCGTCTTCT	2312		
Qy	62	CCCAAAATCAGTCTCTCTTACCCCGCTCTCGATTCTCTCAATATCCCACTATTCTCAGCA	121		
Db	2311	TCGACGTCGTATCGTCTCTCCGTCACCTGGTCTCTCTCACGCCGTACCGTCGTCGGTG	2252		
Qy	122	CCTTCGACGAAGGCTTTAAGCGC	144		
Db	2251	CCGTTGCAAGAAGGAAGGAAGCGC	2229		

```

RESULT 8
US-10-369-493-37751
; Sequence 37751, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37751
; LENGTH: 2400
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
; US-10-369-493-37751

```

	Query Match	2.6%	Score 35.4;	DB 12;	Length 2400;
	Best Local Similarity	56.4%;	Pred. No. 0.89;		
	Matches 66;	Conservative 0;	Mismatches 51;	Indels 0;	Gaps 0;
QY	487	GGCCAAAGATGCGGTGATCCGCTCTACTCTCCAAGCGTGCCTTAACGACCAATTCCAGAA	546		
Dd	1375	GGCCTGTGTCGGCTGGACCTGGCGACGGGAAGTGCGCTGGAACTACCAGTTCCACCAC	1434		
QY	547	GAGGAATAGCGGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAATAAC	603		
Dd	1435	CACGCTCTCCGACATGCGACCTGCGCACATCTGCAACCTGCTGGACATGAAGAACC	1491		

RESULT 9
US-10-184-644-352/c
; Sequence 352, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-352

Query Match 2.6%; Score 35.2; dB 15; Length 837;
Best Local Similarity 12.6%; Pred. No. 0.6;
Matches 52; Conservative 120; Mismatches 242; Indels 0; Gaps 0

```
Db 675 GWH.MWSC..YHGCTD.GYC.BGSSSH.SG.ACHBY...BRRC.TYT.GA.MG.H. 616
QY 895 ATGGTGTCTGCAACAACACTACCGAGCTTCTTCAAAACATGACCTACCAACTCGACC 954
Db 615 .TBCARY.BWHK.C..SM..HAYDNRTTG...Y.A.TSCA.GH.ANGSY.YAYYC.GRMC 556
QY 955 ATCGCGAAATCGCAACAGAGTCACTCGCGCAACAGACATCAGCGCTTCGTTCAAACTC 1014
Db 555 CNY.B.YAGHYSS..BCCGAYSGHW.CW.CWCCT...N.H...HKD.GYCCKGT.T.C 496
QY 1015 GACCCGCGCATCGCGCAGCGCAAGAGGCTCTCGCGAGCTTCTGCAACAACACCC 1074
Db 495 G.ACHTW.SDMA.GKTDEN.DCSGW.TTG.....GDYSH.C.A..G.YHTRHMC..AB 436
QY 1075 GACAGTCAAGCTATCCTGACGCTGATCGGCTGATCGGACCATCTACCAAGCTCATGCTGAGT 1134
Db 435 .D..T..MH..GDCRCH..HA..YTS.G.SW....HBDTKB.TKBDYSAS..CN.S.G. 376
QY 1135 TCTTGGCGCAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGTAAGCCCGAG 1194
Db 375 MSNHD.KN.BDC..DTTA.TS..CHH.B.TGSYT.HGBACBHTKC.AHGASBCG.H.YA. 316
QY 1195 ACTGTGAGCGCAATCTTTGAGCCTCTTGAGAGCTTGATGCTACTTTATGCC 1248
Db 315 ..TAH.DH.CSH..AN.CV.WTG.SY.A.TTS.CB..C..CSC..B.YABB.SB 262
```

RESULT 10

```
US-10-184-634-352/c
; Sequence 352, Application US/10184634
; Publication No. US2003006864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-352
```

```
Query Match 2.6%; Score 35.2; DB 15; Length 837;
Best Local Similarity 12.6%; Pred. No. 0.6;
Matches 52; Conservative 120; Mismatches 242; Indels 0; Gaps 0;

QY 835 GAAAGATCGATGCTCTGCACTACCGAGTCTTCTGCGTGTGATGCTCGACCGCA 894
Db 675 GWH.MWSC..YHGCTD.GYC.BGSSSH.SG.ACHBY...BRRC.TYT.GA.MG.H. 616
QY 895 ATGGTGTCTGCAACAACACTACCGAGCTTCTTCAAAACATGACCTACCAACTCGACC 954
Db 615 .TBCARY.BWHK.C..SM..HAYDNRTTG...Y.A.TSCA.GH.ANGSY.YAYYC.GRMC 556
QY 955 ATCGCGAAATCGCAACAGAGTCACTCGGCGCAACAGACATCAGCGCTTCGTTCAAACTC 1014
Db 555 CNY.B.YAGHYSS..BCCGAYSGHW.CW.CWCCT...N.H...HKD.GYCCKGT.T.C 496
```

```
QY 1015 GACCCGCGCATCGCGCAGCGCAAGAGGCTCTGCGAGCTACTCTGCAACAACACCC 1074
Db 495 G.ACHTW.SDMA.GKTDEN.DCSGW.TTG.....GDYSH.C.A..G.YHTRHMC..AB 436
QY 1075 GACAGTCAAGCTATCCTGACGCTGATCGGCTGATCGGACCATCTACCAAGCTCATGCTGAGT 1134
Db 435 .D..T..MH..GDCRCH..HA..YTS.G.SW....HBDTKB.TKBDYSAS..CN.S.G. 376
QY 1135 TCTTGGCGCAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGTAAGCCCGAG 1194
Db 375 MSNHD.KN.BDC..DTTA.TS..CHH.B.TGSYT.HGBACBHTKC.AHGASBCG.H.YA. 316
QY 1195 ACTGTGAGCGCAATCTTTGAGCCTCTTGAGAGCTTGATGCTACTTTATGCC 1248
Db 315 ..TAH.DH.CSH..AN.CV.WTG.SY.A.TTS.CB..C..CSC..B.YABB.SB 262
```

RESULT 11

```
US-10-063-685-24/c
; Sequence 24, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,685
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 24
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-685-24
```

```
Query Match 2.6%; Score 35; DB 13; Length 556;
Best Local Similarity 7.4%; Pred. No. 0.56;
Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;
```

```
QY 525 CCGTAACGACCCATTACCGAGAGGAAATGACGCCATGAACTCGATCGCAAGCAT 584
Db 509 S.G..R.GCSCSC.CSS.HS.H..HBHNCNRTNNKMSAKBY.TK.Y....H.MSAHB.B 450
QY 585 AGTTCTTACCTTGAAACTATACGATTGGCCCGAGGTAGATCATCATGTTCAAGC 644
Db 449 .NNC.NT.CNCABT..RYSMCMNWGHH.NCNCITKY.HNGENS..SSW.MMT.M.M.M 390
QY 645 TGATGTAGCTGGTGGTGACGCTGTTCTCACGCGGTGAGTCAAGCTGGGGTCTTCCAC 704
Db 389 BHAB.YH.SACTAA.Y...DD.Y.YTS.TS.S.SYS.YCT...M..CGC..BM.SB.BS 330
QY 705 ATTGAGCCCCAAGCCATGTCAGAGTCAAGGATGCTGCTACCAAGACTCTTGACGATC 764
Db 329 NH.KNK.THS.MBH..HKBS..N..C.Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270
QY 765 AACAAATGCTGCTGACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCTCTCG 824
Db 269 KRG.MEAB..CYGDSGR.KM..TDAG.TA.NBBSBMSBHCITB.T.C.T.AYTTB.TYAB. 210
QY 825 CGTGCCTCTCGAAGAAATCGATGCTCTGACCTCTGACCTACCGAGTCTTCTGCGTCTGTGATGC 884
Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K...NBNCBBR 150
QY 885 TCGACCGGCAATGGGTGCTCTCGAACAACATACCCAGGCTTCTTCAAAACATGACCTACCA 944
```

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMYST.BT...DNG. 90

QY 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 12

US-10-184-644-136/c

; Sequence 136, Application US/10184644

; Publication No. US2003004930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P430R1C227

; CURRENT APPLICATION NUMBER: US/10/184,644

; CURRENT FILING DATE: 2002-06-28

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 136

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-644-136

Query Match 2.6%; Score 35; DB 15; Length 556;

Best Local Similarity 7.4%; Pred. No. 0.56;

Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;

QY 525 CGTAAAGCCATTCACCAAGAGAAATGACGGCCATGACATCGATCGAAGCAT 584

Db 509 S.G..R.GCSCS.CSS.HS.H..HBHNCNRTNMKSAKEY.TK.Y....H.MSAHB.B 450

QY 585 AGTTCCTTACTTGAAACTATACGATGGCCCGAGGTAGATCATCAGATTGTCAAAGC 644

Db 449 .NNC.NT.CNCABT..RYSMCMNWGHH.NCNCCTTKY.HNGENS...SSW.MMT.M.M.M 390

QY 645 TGATGTAGCTGGTGGTACGCTGTTCTCAGCCCGGTGACGAGTGGGGGTTCTTAC 704

Db 389 BHAB.YH.SACTTAA.Y...DD.Y.YTS.TS.S.YCT...M..CGC..BM.SB.BS 330

QY 705 ATTCAGCCCCAAGCCATGTCAGAGTCAAGGATGCTGCTACCAAGACTCTTGACGATC 764

Db 329 NH.KNK.THS.MBH..HKBS..N..C..Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270

QY 765 AACAAAGTCTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 824

Db 269 RNRG.MBAB.CYDGSGR.KM..TDAG.TA.NBBSBMSBHCTBT.C.T.AYTTB.TYAB. 210

QY 825 CGTGGCTCGAAGAAATCGATGCTGTCGACCTACGAGTTCGCGCTGCTGATGC 884

Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K..NENCBHR 150

QY 885 TCGACCGGCAATGGTGTCTCGAACAATACCCAGGCTTCTTCAAACATGACCTACCA 944

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMYST.BT...DNG. 90

QY 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 14

US-10-374-780A-932

; Sequence 932, Application US/10374780A

; Publication No. US2004001927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

RESULT 13

US-10-184-634-136/c

; Sequence 136, Application US/10184634

; Publication No. US2003006884A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P430R1C217

; CURRENT APPLICATION NUMBER: US/10/184,634

; CURRENT FILING DATE: 2002-06-28

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 136

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-634-136

Query Match 2.6%; Score 35; DB 15; Length 556;

Best Local Similarity 7.4%; Pred. No. 0.56;

Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;

QY 525 CGTAAAGCCATTCACCAAGAGAAATGACGGCCATGACATCGATCGAAGCAT 584

Db 509 S.G..R.GCSCS.CSS.HS.H..HBHNCNRTNMKSAKEY.TK.Y....H.MSAHB.B 450

QY 585 AGTTCCTTACTTGAAACTATACGATGGCCCGAGGTAGATCATCAGATTGTCAAAGC 644

Db 449 .NNC.NT.CNCABT..RYSMCMNWGHH.NCNCCTTKY.HNGENS...SSW.MMT.M.M.M 390

QY 645 TGATGTAGCTGGTGGTACGCTGTTCTCAGCCCGGTGACGAGTGGGGGTTCTTAC 704

Db 389 BHAB.YH.SACTTAA.Y...DD.Y.YTS.TS.S.YCT...M..CGC..BM.SB.BS 330

QY 705 ATTCAGCCCCAAGCCATGTCAGAGTCAAGGATGCTGCTACCAAGACTCTTGACGATC 764

Db 329 NH.KNK.THS.MBH..HKBS..N..C..Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270

QY 765 AACAAAGTCTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 824

Db 269 RNRG.MBAB.CYDGSGR.KM..TDAG.TA.NBBSBMSBHCTBT.C.T.AYTTB.TYAB. 210

QY 825 CGTGGCTCGAAGAAATCGATGCTGTCGACCTACGAGTTCGCGCTGCTGATGC 884

Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K..NENCBHR 150

QY 885 TCGACCGGCAATGGTGTCTCGAACAATACCCAGGCTTCTTCAAACATGACCTACCA 944

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMYST.BT...DNG. 90

QY 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 14

US-10-374-780A-932

; Sequence 932, Application US/10374780A

; Publication No. US2004001927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

```
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Onaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 932
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G568
US-10-374-780A-932

Query Match          2.6%; Score 34.6; DB 12; Length 427;
Best Local Similarity 50.3%; Pred. No. 0.67;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 11 AGATACAGCTCGACACCCCTCGGCAGCTACCGAGCCCTCCCTTCGATCTACACCCCAATCA 70
Db 2 AAAAAATGCACACAGCACAAGTCCCAACCAATATTCCTTCGATCTTAACCTTGTACT 61

Qy 71 GTCTCCTCTACCCGCTCTCTGATTCCTCAATATCCCACTATTGTTCAGACCTTCGAGC 130
Db 62 GCTACTGCTACCAACAATATTAATCTATATATTTCAITTCCTTCGCCCCCTTCAGAA 121

Qy 131 AAGTCTTAAGCGCTTCTCGGAAGCCGCTCCCATGGTGCAGGCCAGGT 179
Db 122 TTGGGTGGATGAGGTTCCTCCGAAGTGAGCTCTTGTTGGGAGGACCAAT 170
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RESULT 15
US-10-027-632-31187
; Sequence 31187, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31187
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-31187

Query Match          2.6%; Score 34.6; DB 13; Length 1112;
Best Local Similarity 51.6%; Pred. No. 1.1;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 941 ACCACAACTCGACCATCGCGGAAATCGCAACGAGTCACTCGGCGCAACAGCATCACGCC 1000
Db 867 ATCACACCTGATCTACTGAGCACTCAATTCCTCTCACTCAGACCCACAGCCAGTGCC 926

Qy 1001 TTGTTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGAACAAGAGTCTCGCGACGTACC 1060
Db 927 GGAGTTATCGCGTGGAAACCCCTCGGACCCACAGCCAGTTCAGAGTTATCGCGTGGAAAC 986

Qy 1061 TGACACAAACCCCGCAAGTCCCAACGTATCCC 1093
Db 987 CTCGGACCCACAGCCAAAGTCCCGGATTTATTCAC 1019
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Search completed: February 7, 2004, 23:31:24
Job time : 532 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:53:23 ; Search time 94 Seconds
(without alignments)
6367.186 Million cell updates/sec

Title: US-10-614-954-5
Perfect score: 1356
Sequence: 1 atggcttcaagatacacgct.....atggcagtaagttggttag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA.*

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- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
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- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1356	100.0	1356	4	US-09-538-414-5
2	915.6	67.5	1403	4	US-09-538-414-1
3	915.6	67.5	12949	4	US-09-538-414-11
4	915.6	67.5	13737	4	US-09-538-414-10
5	249.8	18.4	1425	4	US-09-538-414-7
6	39.8	2.9	4403765	3	US-09-103-840A-2
7	39.8	2.9	4411529	3	US-09-103-840A-1
8	34.2	2.5	720	4	US-09-252-991A-16032
9	34.2	2.5	1074	4	US-09-252-991A-16568
10	34.2	2.5	2721	4	US-09-252-991A-16144
11	33.4	2.5	516	4	US-09-252-991A-15293
12	33.4	2.5	1614	4	US-09-252-991A-15438
13	32.8	2.4	1230025	4	US-09-198-452A-1
14	32.4	2.4	1620	4	US-09-125-642C-9
15	32.4	2.4	1740	4	US-09-125-642C-2
16	32.4	2.4	1742	4	US-09-125-642C-13
17	32.4	2.4	5515	4	US-09-125-642C-8
18	32.4	2.4	5519	4	US-09-125-642C-12
19	32.2	2.4	1482	4	US-09-252-991A-8923
20	32.2	2.4	1782	4	US-09-252-991A-9072
21	32.2	2.4	2121	4	US-09-252-991A-9159
22	32	2.4	1406	4	US-09-699-266A-10
23	31.4	2.3	1482	4	US-09-252-991A-1338
24	31.4	2.3	1671	4	US-09-252-991A-1222
25	31.4	2.3	1917	4	US-09-252-991A-1386
26	31.4	2.3	2190	2	US-08-492-027A-7
27	31.2	2.3	456	4	US-09-252-991A-6665

C	28	31.2	2.3	480	4	US-09-410-551B-64	Sequence 64, Appl
C	29	31.2	2.3	1611	4	US-09-252-991A-6694	Sequence 6694, Ap
C	30	31.2	2.3	2577	4	US-09-252-991A-6607	Sequence 6607, Ap
C	31	31.2	2.3	4466	4	US-09-410-551B-20	Sequence 20, Appl
C	32	31.2	2.3	9862	4	US-09-691-861A-3	Sequence 3, Appli
C	33	31.2	2.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
C	34	31	2.3	5183	1	US-08-459-568-3	Sequence 3, Appli
C	35	31	2.3	5183	2	US-08-399-411-3	Sequence 3, Appli
C	36	31	2.3	5467	2	US-08-605-106-7	Sequence 3, Appli
C	37	31	2.3	5868	3	US-08-516-859A-3	Sequence 7, Appli
C	38	31	2.3	5868	4	US-09-586-472-3	Sequence 3, Appli
C	39	31	2.3	5868	4	US-09-528-706-3	Sequence 3, Appli
C	40	30.6	2.3	1263	4	US-09-252-991A-10039	Sequence 10039, A
C	41	30.6	2.3	1353	4	US-09-252-991A-9985	Sequence 9985, Ap
C	42	30.6	2.3	1569	4	US-09-252-991A-9806	Sequence 9806, Ap
C	43	30.4	2.2	480	4	US-09-410-551B-68	Sequence 68, Appl
C	44	30.4	2.2	1710	4	US-09-252-991A-7942	Sequence 7942, Ap
C	45	30.4	2.2	2718	4	US-09-252-991A-7538	Sequence 7538, Ap

ALIGNMENTS

RESULT 1

US-09-538-414-5
; Sequence 5, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538.414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-09-538-414-5

Query Match	100.0%;	Score 1356;	DB 4;	Length 1356;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTTCGATCTAC	60	
Db	1	ATGGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACAGGGCTCTCTTTTCGATCTAC	60	
QY	61	ACCCAAATCAGTCTCTCTTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTCAGC	120	
Db	61	ACCCAAATCAGTCTCTCTTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTCAGC	120	
QY	121	ACCTTCGAGCAAGGCTTTAAGCGCTTCTCGAAGCGGTCCCATATGGGTCCGAGGGCAGGTC	180	
Db	121	ACCTTCGAGCAAGGCTTTAAGCGCTTCTCGAAGCGGTCCCATATGGGTCCGAGGGCAGGTC	180	
QY	181	AAAGCCGAGGCGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC	240	
Db	181	AAAGCCGAGGCGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC	240	
QY	241	GTTCCTCGTGTTCGTAGTGAAGACCTTCGCGATGATCTTCAGCGGCCCAACCATCGAGGTT	300	
Db	241	GTTCCTCGTGTTCGTAGTGAAGACCTTCGCGATGATCTTCAGCGGCCCAACCATCGAGGTT	300	
QY	301	ATGAGAAAGCGGGGATACCCCTATGGCGATGTTTGAAGAGAACTATCGCGCCCAAGGAAG	360	

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753 CTCGGAGCTGAAGACGAGCAACAAAGACTCTTGACGCGTGTCAAGTTTGTGTCAAC 812
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Qy | | | | |
783 TGACGATGCTCTTTTCGGGTTTTCATCTGAAATCGGCTCTCGCGTGCCTCTCGAAGAAT 842
| | | | |
Db | | | | |
813 TGATGATGCTCTTTTCGGGTTTTCATCTGCAATCAACCTCGGCGTGAAGTCTCGCAAGAT 872
| | | | |
Qy | | | | |
843 CGATGGCTCTGACCTACGAGTTCTGCGGTGTGTGATGCTGCAACGGCAATGGGTGT 902
| | | | |
Db | | | | |
873 GGATGCTTTCCACACTACTGAATTTCTGCGGCTGTGACATGCGGGCCCAATGGGGT 932
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Qy | | | | |
903 CTCGAAACAACTACCGAGCTTTCTTCAAAAGATGACCTTACACACTCGACATCGGCGA 962
| | | | |
Db | | | | |
933 ATCAAGCAATACCGAGGCTTTCTTCAAAATGATGACCTTACCATGACTCGACCGTGGCGA 992
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Qy | | | | |
963 AATCGCAACAGTACTCTCGGCGCAACAGCATCACGCTTCTGTTTCAAGACTCGACCCCGC 1022
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Db | | | | |
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Qy | | | | |
1023 GAGCATGGCGAGCAACAGAGTCTCGGAGTACCTGCAACAAACCCCGCAAGTGC 1082
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1053 TCGTTTGGCGAGAGCAACAAAGCTTTGGCGAGCTTACATGATGCTGCTGCAAGTGC 1112
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1083 CAAGTATCCCTGACGCTGAGTGGGACCACTTACCAGGCTCATGCTGAGTTCTTGGGC 1142
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1113 GAGGCTCTCCCTGACCGCGGAGTCCGATCCGTCGAAGCAGCATCATGCTGAGTTCTTGGGC 1172
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1143 CAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGGGTAAAGCCGAGACTGTGAG 1202
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1173 CAAGTGGGATGCTGGGAGTATGACTTTGGTTTGGACTGGTAAAGCTGAGTGTGAG 1232
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1203 ACGGCCAATCTTGAAGCTGTGAGAGCTTGAATGATCTTTATGCCAAGAGCCCTGATGG 1262
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1233 AAGACCTCGCTTTGAACTTTGAGAGTTTGAATGATCTTTATGCCAAGAGCCCTGATGG 1292
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Qy | | | | |
1263 CGAGTCTGTGCGCGCTTCTCTGAGGATGAGATGATGACCGATGAGGCGGATAA 1322
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1293 GGAGTTTACGCGCTTCAATTTCTGAGGATGAGGATGAGAGACTTAAAGGCGGATGA 1352
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1323 GGAGTGACCAAGTATGCGAGTACGTTGTTGTTAG 1356
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1353 GGAGTGACCAAGTATGCGAAGTATTTGGTGTAG 1386
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RESULT 3

US-09-538-414-11
; Sequence 11, Application US/09538414
; Patent No. 6346655

GENERAL INFORMATION:
; APPLICANT: Hohm, T.

; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list

; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11
; LENGTH: 12949

; TYPE: DNA
; ORGANISM: Plasmid

US-09-538-414-11

Query Match 67.5%; Score 915.6; DB 4; Length 12949;
Best Local Similarity 80.3%; Pred. No. 1.3e-281;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

Qy 3 GGCTTTCAAGATA CAGCTCGACACCCCTCGGCAGCTACAGGCTCTCTTTGATCTACAC 62
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Qy 63 CCAATCAGTCTCTCTACCCGCTCTGATTCCTCTCAATATCCACTATTTGTCAGCAC 122
| | | | |
Db 11341 CCAGATCAGTCTCGTTTACCCGCTCTGATTCCTTCCAGTATCCACCATGTCAGCAC 11400
| | | | |
Qy 123 CTTGAGCAAGGTCTTAAGCGCTTCTCGAAAGCGTCCCATGGGTGCGAGGCCAGTCAA 182
| | | | |
Db 11401 CTTTGAAGAGGCTTAAACCGCTCTCTCAAACTTCCCATGGGTGCGGGCCAGTCAA 11460
| | | | |
Qy 183 AGCCGAGGCAATGAGCGAGGAAACACAGAACTTCCCTTTATCGTCCCTTTTGAAGAGT 242
| | | | |
Db 11461 GACCGAGGCAATGAGCGAGGAAACACAGAACTTCCAAAGATCATTCATATGAGGAGAC 11520
| | | | |
Qy 243 TCCTCGTGTGTAGTGAAGAGCTTCCGCGATGATCTTTCAGGCGCCAGATCGAGGTAT 302
| | | | |
Db 11521 ACCCGCTCTTGTGTGAAGAGCTTCCGCTGATTTCTTCAAGATCATTCATATGAGGAGT 11580
| | | | |
Qy 303 GAGAAAGCGCGGATACCTATGCGGATGTTTGAAGAGAACTCATCGCGCCAGGAAACAC 362
| | | | |
Db 11581 GAGAAAGCGGCTTTCCTTAGAGATGTTTGAAGAGAACTCATCGCGCCAGGAAACAC 11640
| | | | |
Qy 363 GTTACCTATTGGAACCTGCTACTGTCGCGAGCAACCCAAAGCTGTAAATTTATTTGACGT 422
| | | | |
Db 11641 ATTAGCTATCGGACTGCGCAATGCGCCCAACGACCGAAGCTGTGTGCTATTGCACT 11700
| | | | |
Qy 423 CAACCTTCAAGGCGGAGCTCATCTCCTACTGTCTCAACGAGCAGCAGTGTCTGATAT 482
| | | | |
Db 11701 CAACCTTCAAGGCGGAGCTCATCTCCTACTGTCTCAACGAGCAGCAGTGTCTGATAT 11760
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Qy 483 GGTAGGCAAGATGCGGTGATCCGCTACTCTCAAGCGGTGCGTAACGACCCATTCCAC 542
| | | | |
Db 11761 GACAGGACAGATGCAATTAATTTCTCTTCTTCAAGCGGTGCGTAACGATCATTTCC 11820
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Qy 543 CGAAGAGAAATGACGCGCATGAACCTCGATCGCAAGACGATAGTTCTTACCTTTGAAAA 602
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Db 11821 CGAGGAGAAATCTCGGCCATGAACCTCGATCGCAAGACGCTAGTCTCTCTTTGAAA 11880
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Qy 603 CTATACGATTTGGCCCGGAGGTAGTATCATCATGATGTTCAAGCTGATGATGTTGTTGA 662
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Db 11881 CTACAAAGTTGTTGCTGAGCTAGACCAACAGATGCGCAACCC--TGGCGCTGCTGGCGA 11937
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Qy 663 CGCTGTTTCTCACGCGGTGAGTCAAGCTGGCGTCTTTCACATTCAGCCCAAGGCGAT 722
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Db 11938 CGCTCCACCGCACCGGCAAGCAAGCTGGCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 11997
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Qy 723 GTCAGAGCTCAAGATGCTGCTACCAAGACTCTTGAAGCACTCAACAAAGTTCTGTGTGAC 782
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Db 11998 CTCGGAGCTGAAAGACGACGCAAAAGACTTTGAGCGCTGCTCAAGTTTGTGTCAAC 12057
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Qy 783 TGAGATGCTCTTTTCGGGTTTCAATCTGGAATCGGCTCTCGGCTGCTGCTGCTGCTGCTG 842
| | | | |
Db 12058 TGATGATGCTCTTTTCGGGTTTCAATCTGGAATCAACCTCGCGCTGCTGCTGCTGCTGCTG 12117
| | | | |
Qy 843 CGATGCTCTGCACTTACCGAGTTCTTCCGCTGCTGTTGATGCTGCAACCGGCAATGGTGT 902
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Db 12118 GGATGCTTCCACACTTACTGAAATCTGCGCGCTGTGACATGCGGGGCCAATTTGGCGGT 12177
| | | | |
Qy 903 CTGAAACAACTACCCAGGCTTCTTCAAAACATGACCTTACCAACTCGACCTCGGCGCA 962
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Db 12178 ATCAAGCACATACCCAGGCTTCTTCAAAACATGACCTTACCATGACTCGACCGTGGCGA 12237
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Qy 963 AATCGCAACAGTACTCGGCGCAACAGATCATCGCTTCTGTTTCAAGACTCGACCCCGC 1022
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Db 12238 AATCGCAACAGTACTCGGCGCAACAGATCATCGCTTCTGTTTCAAGACTCGACCCCGC 12297
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Qy 1023 GAGCATGGCGAGCAAGAGTCTCGGAGGATGCTCGGAGGATGCTGCAACAAACCCGAGTGC 1082
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Db 12298 TCGTTTGGCGAGCAAGCAAGCTTTGGCGAGTATGATGATGCTGCTGCTGCTGCTGCTGCTG 12357
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QY 1083 CAACTATCCCTGAGCGGTGATGCGGACCACTACACAGGCTCATCTGAGTCTTTGGGC 1142
DB 12358 GAGCGTCTCCCTGACCGCGGATCGGATCCGTCAGCAGATCATCTGAGTCTTGGGC 12417
QY 1143 CAAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGGACTGGGTAAGCCGAGACTGTGAG 1202
DB 12418 CAAAGTGGGATGCTGGGATGATGACTTTGGGTTGGACTGGGTAAGCCCTGAGAGTGTGAG 12477
QY 1203 AGCGCAATCTTTGAGCCCTGTTGAGAGCTGTGATGATCTTTATGCCCCAAGAGCCCTGATGG 1262
DB 12478 AAGACCTCGCTTTGAACCTTTTGGAGAGTTTGTATGTTATGCCCCAAGAGCCCTGATGG 12537
QY 1263 CGAGTTCTGTGGCGCTTCTCTGAGGGATGAGGATGCGACCGATTGAAGCGCGATAA 1322
DB 12538 GGAGTTTACGGCGTCCATTTCTCTGAGGGATGAGGATGCGAGACTAAGCGCGATGA 12597
QY 1323 GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
DB 12598 GGAGTGGACCAAGTACGCAAGTATATGGGTAG 12631

RESULT 4
US-09-538-414-10
; Sequence 10, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-538-414-10

Query Match 67.5%; Score 915.6; DB 4; Length 13737;
Best Local Similarity 80.3%; Pred. No. 1.3e-281;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACGAGGCTCTTCGATCTACAC 62
DB 50 GTCTTTTGACATAGAGCTGACATCATCGGCGAGCAACCGCTCTTCTTTCAATCTACAC 109
QY 63 CCAATCAGTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTTGAGCAGAC 122
DB 110 CCAGATCAGTCTCTTTTACCCGCTCTGATCCCTCCAGTATCCCACTCTGTCAGCAGAC 169
QY 123 CTTTCGACAGGCTTTAAGCGCTTCTCCGAGCGCTCCCATGGGTGCGAGGCCAGGTCAA 182
DB 170 CTTTGGAGAGGCCCTAAACCGCTCTCTCAACCTTCCCATGGGTGCGGSCCAGGTCAA 229
QY 183 AGCCGAGGCAATGACGAGGGAACACAGAACTTCTTTATCGTCCCTTTTGGAGGCT 242
DB 230 GACCGAGGCAATGACGAGGGAACACAGAACTTCTCAAGATCATTCATATGAGGAGAC 289
QY 243 TCCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGCCCGATCGAGGATAT 302
DB 290 ACCCGCTGTGTGTGAAGACCTTCGCGTGTGATTCCTCAGCGCCCAAGATCGAGGGTT 349
QY 303 GAGAAAGCGGGAATACCTTATGGGATGTTTGAAGAGAACTATCATCGGCCCAAGGAAGAC 362

DB 350 GAGAAAGCGGCGTTTCCCTTAGAGATGTTTGAAGAAACGTCGTCGCTCCGAGGAAGAC 409
QY 363 GTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGACCTGTATTTCTATTGTCAGCT 422
DB 410 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCTGTGTGCTATTGTCAGCT 469
QY 423 CAACTTTCATCAAGGGCGGACTCATCTCTCATCTGTCAACGAGCAGCAGGTCGTATGATAT 482
DB 470 CAACTTTCATTAAGGGCGGACTCATCTCTCAACCGTCAACGAGCAACATGGTGTATGACAT 529
QY 483 GGTAGGCAAGATGCGGTGATCCGTCTACTCTCCAAAGGGGTGCGGTAAAGACCACTTTCAC 542
DB 530 GACAGACCAAGATGCAATTTATTCGTCTCTCCAAAGGGGTGCGGCAACGATCATTTTCAC 589
QY 543 CGAAGAGGAAATGACCGCCATGAACCTCGATCGCAAGACGATAGTTTCTTTACCTTGAATA 602
DB 590 CGAGGAGGAAATCTCGCCCATGNAACCTCGATCGAAGACGGTAGTCCCTCTCTCTTGAATA 649
QY 603 CTATACGATTTGGCCCGAGGTAGATCATCAGATTTGTCAAAGCTGTAGCTGTGTGTGTA 662
DB 650 CTACAAAGTTGGTCTCTGAGCTAGACCAACGATCGCAAAACC--TGCGCTCTCTGGCGA 706
QY 663 CGCTGTTCTCACCGCCGTCAGTCAAGCTGGGCGTTCTTCACTTCAGCCCCCAAGGCCAT 722
DB 707 CGCTCCACCGGCAACCGCCAAAGCAAGCTGGGCGTTCTTTTCAITCACTCCCAAGGCCCT 766
QY 723 GTCAGAGCTCAAGGATGTCTTACCAAGACTCTTGAACGATCAACAAAGTTCGTGTGAC 782
DB 767 CTCGAGCTGAAAGACGACGACCAAAAGACTCTTGAACGCTCGTCCAAAGTTTGTGTCAAC 826
QY 783 TGACGATGCTCTTTTGGCGGTTCACTGTGAAATCGGCTCTCGGCTGTGCTCGAAGAAT 842
DB 827 TGATGATGCTCTTTTGGCGGTTTATCTGGCAATCAACCTCGCGGTAGCTCTCGCAAGATT 886
QY 843 CGATGCTCTGACCTACCGAGTCTTGGCTGTGTGTGATGCTCGACCGCAATGGTGT 902
DB 887 GGATGCTTCCACACTACTGAACTTCTGCGCGGTGTGCAATCGGGGGCCCAATGGCGT 946
QY 903 CTCGAAACAATACCCAGGCTTCTTCAAAAACATGACCTACCAAACTCGACCATCGCGCA 962
DB 947 ATCAAGCAATACCCAGGCTTCTTCAAAACATGACCTACCAATGACCTCGACCGTCCGCA 1006
QY 963 AATCGCCAAAGCTCTCGGCGCAACAGCATCAGGCTTCTGTTTCAAGACTCGACCCCGC 1022
DB 1007 AATCGCCAAAGCAACCACTTGGCGCAACAGCATCAGGCTCTGCTCGGTAACCTCAACAGTGA 1066
QY 1023 GAGATGCGCCGAGCAAGAGGCTCTCGGAGCTTCTGCAACAACCCCGCAAGTC 1082
DB 1067 TCGTTTTCGCGAGACGACCAAGCTTTGGCGAGGTAATGATGCTGCGCTGCTGCAAGTC 1126
QY 1083 CAACTATCCCTGACGCGCTGATGCGGACCCATCTTACCAGGCTCATGTGAGTCTTGGGC 1142
DB 1127 GAGGCTCTCTGACCGCCGATCGAATCCGTCAAGCAGCATCATGTGAGTCTTGGGC 1186
QY 1143 CAAAGTGGGACTCTGGGATTAAGCTTTGGGCTCGGCTCGGTAAGCCCGAGACTGTGAG 1202
DB 1187 CAAAGTGGGATGCTGGGATGATGACTTTGGGTTTGGACTGGTAAGCTCTGAGGTGTGAG 1246
QY 1203 ACGGCCAATCTTTGAGCTGTGAGGCTTGAAGCTTGAATGCTTATGCGCAAGAGCCGTGAG 1262
DB 1247 AAGACCTCGCTTTGAACCTTTTGAAGTGTGATGATCTTTATGCGCCCAAGAGCCGTGAG 1306
QY 1263 CGAGTCTGTGGCGGCTTCTCTGAGGATGAGGATATGACCGATTGACCGGCGGATAA 1322
DB 1307 GGAGTTTACGGCTCCATTTCTTGAAGGATGAGGATGAGGATGAGGAGACTTAAAGCGGATGA 1366
QY 1323 GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356
DB 1367 GGAGTGGACCAAGTATGCGCAAGTATATTGGGTAG 1400

; Sequence 7, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-7

Query Match 18.4%; Score 249.8; DB 4; Length 1425;
Best Local Similarity 51.9%; Pred. No. 1.5e-69;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGCTGACACCTCGGCGACGCTACGAGCGCTCTCTTTCGATCTACACCCAAATCAGTCTC 75
Db 64 CAACCTGATATTTTGGGACAAACAGCTTCGCTATACAACTATACACTCAATATGCTCT 123

QY 76 CTCACCCCGCTCTGATTCCTCTCAATATCCACTATTGTCAGACCTTCGACAGGT 135
Db 124 ATCTACCGTGTACGATCTCTCTGCTCATGACCATATCGTAATATCTTAAACAGAGA 183

QY 136 CTTAAGCGCTTCTCCGAGCGCTCCATCGGTGCGAGCCAGGTCAAGCGCGAGCGATT 195
Db 184 CTTGAACATTGGCTAAATAATTTCCAGTGGCTAGCAGGAATGCTGTAATGAGGTCT 243

QY 196 AGCAGGGAACACAGAACTTCCTTATCTGCTGCTTTGAGGAGGTTCCTCGTGTGTA 255
Db 244 GACGAAGGTAACTGCTGCTACAGAAATTTCCCGTCAGACAAAATTCAC---TTATC 300

QY 256 GTGAAAGACCTCCGCGATGATCTTCAGCGCCACGATCGAGGTATGAGAAAGCGGGA 315
Db 301 GTCAGATCTTCGAGAGATCTGCTGCCCCAACAATGAGATTGCTGTGAAAGAGCTGAC 360

QY 316 TACCTATGCGATGTTTGAGGAAACATCATCGCGCCAGGAAGAGCTT-----ACCT 369
Db 361 TTTCTATCTACATGTTAGAGAAAGACTTTTGGCGCTTGCAATGACTATCAATCCACCT 420

QY 370 ATTGGACCTGCTGCTGCGGAGCAGCCAAAGCTGTAATCTTATTTGCGAGCTCAACTTC 429
Db 421 GGAAACATAAGTATGATGCGCGCCAGAGTGGGCTGTATTTGAGTTCAAGCAAACTTT 480

QY 430 ATCAAGCGCGGACTCATCTCCTCAGTCAACGAGCAGCAGCTGCTATGATATGATAGGC 489
Db 481 ATCTCCGGCGGCTTCGCTTAACTATTTGTCGGCAGCACAATATTTGATATACAGGA 540

QY 490 CAAGATCGGTGATCCGCTCTACTCTCAAGCGGTGCGGTAAACGCCCACTCACCGAAG 549
Db 541 CAGGAAAGTATCATCACTGCTCAATTAATTTGCGCAACCAAACTTTCTCTGATGAA 600

QY 550 GAAATGCGGCATGAACCTGATGCGAAGAGATGTTCTTACCTTGAAACATATACG 609
Db 601 GAACTGCTCATTTGAAATATAGATAAAGCAATCTATCTCTTTGTTGATGAACTTGG 660

QY 610 ATT---GGCCCGAGGTGATCATCATGTTCTCAAGCTGATGATGCTGGTGGTGCCT 666
Db 661 GAACCCGACACCGCTAGTTTATGAAATAGTGAACCTCTAGAAATACAGAGTGGAG 720

QY 667 GTTCTACGCGGTCAGT-----GCAAGCTGGGCGTCTTCTCACTTACAGCCCAAG 717
Db 721 GAAAGGAACAGTCTTCTTCTGAACTCTACTTTGGGCTTATGTTGAATTTCTGCTATC 780

QY 718 GCCATGTGAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGATCAACAAAGTTCGTG 777
Db 781 TCAUATGCAAACTCTCAGGATTTGGCAATGACAGATGATCTCTTGGCACAATAATTTGTC 840

QY 778 TCGACTGACGATGCTCTTTTCGGCGTTTCACTGGAATCGGCTCTCGGCTGGTCTCGAA 837
Db 841 TCCACTGATGATATGCTCACTGCTTTTCACTGGAATCAGTTTCTCGAGCCCGTTTATCT 900

QY 838 AGAATCGATGCTCTGCACTACCGAGTCTGCGCGTCTGTGATGCTCGACCGCAATG 897
Db 901 CGACTTAAACAGAAACGAATCAATTTAGGGCTGCTGGAATGTTAGAAACCGGTA 960

QY 898 GGTGCTCGAAACAATACCCAGGCTCTTCAAAACATGACTACCAACTCGACCAATC 957
Db 961 GGAATCCCGGAAACGATATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020

QY 958 GGCAGAAATCGCAACGAGTCACTCGGCGCAACAGATCAAGCTTCGTTGAAACTCGAC 1017
Db 1021 AAAAGCTTGGATCATATAAAGTTTGGGCGTCTTTCATCAGATTCGAGGAAGCTAGAC 1080

QY 1018 CCCGCGAGCA-----TGCGCGAGCAACAGAGTCTCGCGAGTCTCTGCAACAAC 1071
Db 1081 CCTAAAGCTCTCGATTTGGCTATATACATGCGACTTGTAGCTCTCTTACCGATGC 1140

QY 1072 CCCGACAGTCCAAAGTATCCCTGACGCGCTGATGCGGACCATCTTACGAGGCTCATGCTG 1131
Db 1141 CCGGACAGACTAAGGTTTCTATACCTCAACCAATTGATATCTTATCTGGAATTTATGCTC 1200

QY 1132 AGTTCTGGGCGAGGTGGGACTCTGGATTAACAATTTGGGCTCGGACTGGGTAAGCCC 1191
Db 1201 AGTTCTGGGCGAGGTAAGTGGTGTCTATGACGTTGATTTCAATCTAGGCTTTGGGAGCCC 1260

QY 1192 GAGACTGTGAGAGCGCAATCTTTGAGCTCTGAGAGCTTGAATGCTTATGCGCCAG 1251
Db 1261 AAGAGTGTAGAGCGCGCGCTTCATTTCCCTGAGAGCTTAATATTTATGCTTGA 1320

QY 1252 AAGCTGATGCGAGTCTCTGCGCGCTTTCTCTGAGGATGAGGATAGGACCGATTG 1311
Db 1321 TCTTCCAGAGTGAATGGTGTGCTCTTTGCTTAGAGATAAGATTTGGAGTGGCTG 1380

QY 1312 AAGCGGATGAGGATGAGCAACAGTATGC 1340
Db 1381 AATCGGATAAAGAAATGCAAAATTAATGC 1409

RESULT 6

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.9%; Score 39.8; DB 3; Length 4403765;

Best Local Similarity 49.8%; Pred. No. 1.3; Mismatches 102; Indels 0; Gaps 0;
Matches 101; Conservative 0;
QY 956 TCGGCGAAATCCCAACAGTCACTCGCGCGCAACAGCATACGCTTCGTTGAGAACTCG 1015
Db 4219416 TCGAGGAGTTGCGCGCGCCCACTCGAAGCCAGCGCAATCGCTACGCGATATCC 4219475
QY 1016 ACCCGCGAGCATGCGCGCGAGCAACAGAGGTTCTCGGAGTACCTGCAACAAACCCCG 1075
Db 4219476 ACGCCACAGCATCGCGAACTCGAAGATGGTCTGGCCCCGGAACCTGCGGAGGAGCTCG 4219535
QY 1076 ACAAGTCCAACTATCCCTGACGGCTGATCGCGACCCATCTACACGCGTCATCTGAGTT 1135
Db 4219536 ACGGCTTACCTGCGCTTCAACAGAGACGCCGTGCGCTCGGAGCGGAGTTGCGCATTC 4219595
QY 1136 CTTGGGCCAAGTGGGACTCTGG 1158
Db 4219596 CCCAGGCACAGCTGGTGGGCTGG 4219618
RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
Query Match 2.9%; Score 39.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 1.3; Mismatches 102; Indels 0; Gaps 0;
Matches 101; Conservative 0;
QY 956 TCGGCGAAATCGGCAAGTCACTCGCGCGCAACAGCATACGCGCTTCGTTGAGAACTCG 1015
Db 4227170 TCGAGGAGTTGCGCGCGCCCACTCGAAGAGCCAGCGCAATCGGCTAGCGATATCC 4227229
QY 1016 ACCCGCGAGCATGCGCGCGAGCAACAGAGTCTCGGAGAGTACTCTGCACAAACCCCG 1075
Db 4227230 ACGCCACAGCATCGCGGAACTCGAAGATGTTCTGGCCCCGGAACCTGCGGAGGAGCTCG 4227289
QY 1076 ACAAGTCCAACTATCCCTGACGGCTGATCGCGACCCATCTACACGCGTCATCTGAGTT 1135
Db 4227290 ACGGCTTACCTGCGCTTCAACAGAGACGCCGTGCGCTCGGAGCGGAGTTGCGCATTC 4227349
QY 1136 CTTGGGCCAAGTGGGACTCTGG 1158
Db 4227350 CCCAGGCACAGCTGGTGGGCTGG 4227372

RESULT 8
US-09-252-991A-16032
; Sequence 16032, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16032
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16032
Query Match 2.5%; Score 34.2; DB 4; Length 720;
Best Local Similarity 53.3%; Pred. No. 0.74; Mismatches 72; Conservative 0; Indels 0; Gaps 0;
QY 474 TATGGATATGTTAGGCCAAGATGCGGTGATCGCTTACTCTCCAAAGCGTCCGTTAACGA 533
Db 244 TATGATGCTGGAAGCCAGCAGCGCTGCTTCGGCATCTCGCCGAGACAGCCAGGAAGCT 303
QY 534 CCATTCACGAGAGGAAATGACGGCCATGACCTCGATCGCAAGACGATAGTTCTTAA 593
Db 304 CACCATCACCCTCGGACGAGATGATGCCATCAGCAACAGGTGACCATGTGCCACGTC 363
QY 594 CCTTGAATACTATAC 608
Db 364 CCAGGGCGACACAGAC 378
RESULT 9
US-09-252-991A-16568/c
; Sequence 16568, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16568
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16568
Query Match 2.5%; Score 34.2; DB 4; Length 1074;
Best Local Similarity 53.3%; Pred. No. 0.92; Mismatches 72; Conservative 0; Indels 0; Gaps 0;
QY 474 TATGGATATGTTAGGCCAAGATGCGGTGATCGCTTACTCTCCAAAGCGTCCGTTAACGA 533
Db 864 TATGATGCTGGAAGCCAGCAGCGGCTGCTTCGGCATCTCGCCGAGACAGCCAGGAAGCT 805
QY 534 CCATTCACGAGAGGAAATGACGGCCATGAACTCGATCGCAAGACGATAGTTCTTAA 593
Db 804 CACCATCACCTCGGACGAGATGATGCCATCAGCAACAGGTGACCATGTGCGCCAGTC 745
QY 594 CCTTGAATACTATAC 608
Db 744 CCAGGGCGACACAGAC 730
RESULT 10
US-09-252-991A-16144
; Sequence 16144, Application US/09252991A
; Patent No. 6551795

;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 16144
;; LENGTH: 2721
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16144

Query Match 2.5%; Score 34.2; DB 4; Length 2721;
Best Local Similarity 53.3%; Pred. No. 1.5;
Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 474 TATGATATGCTAGGCCAAGATGCGGTGATCGCTACTCTCCAAAGGGTGGCGTAACGA 533
Db 1854 TATGATCTGGAAGCCAGCAGCGCTCTTGGCATCTCGCGAGACGCCAGGAAGCT 1913

Qy 534 CCCATTACCGAAGAGGAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTA 593
Db 1914 CACCATCACTTCGGACGAGATGAGTGCCATCAGCAACAGGTGAGCCATGTCGCCACGTC 1973

Qy 594 CTTGAAACTATAC 608
Db 1974 CCAGGCGACACGAC 1988

RESULT 11
US-09-252-991A-15293/c
; Sequence 15293, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15293
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15293

Query Match 2.5%; Score 33.4; DB 4; Length 516;
Best Local Similarity 52.5%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 896 TGGGTGTCTCGAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACTCGACCA 955
Db 187 TGGTTCCGCGCAGGGCCAGGAAATCATTTTGTCTGACACGCGCGCTCGCTCGACAC 128

Qy 956 TCGGCGAATGCCAACAGTCACTCGGCGCAACAGCATCAGCTTGTTCAGAACTCG 1015
Db 127 TGCAGGAAGCCCTGACAGCTCGTGGGCGTGAGCGCCCGCTCGTCTGCGCAACGTT 68

Qy 1016 ACCCGCGCAGCATGGCCA 1034
Db 67 GCGCGAGGCTTGGCGA 49

RESULT 12
US-09-252-991A-15438
; Sequence 15438, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15438
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15438

Query Match 2.5%; Score 33.4; DB 4; Length 1614;
Best Local Similarity 52.5%; Pred. No. 2.1;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 896 TGGGTGTCTCGAACAATACCCAGGCTTCTTCAAAACATGACCTACCAACTCGACCA 955
Db 1046 TGGTTCCGCGCAGGGCCAGGAAATCATTTTGTCTGACACGCGCGCTCGCTCGACAC 1105

Qy 956 TCGGCGAATGCCAACAGTCACTCGGCGCAACAGCATCAGCTTGTTCAGAACTCG 1015
Db 1106 TGCAGGAAGCCCTGACAGCTCGTGGGCGTGAGCGCCCGCTCGTCTGCGCAACGTT 1165

Qy 1016 ACCCGCGCAGCATGGCCA 1034
Db 1166 GCGCGAGGCTTGGCGA 1184

RESULT 13
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (15001)-(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (30001)-(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (45001)-(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (60001)-(75000)
; OTHER INFORMATION: n=a or c or g or t


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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (810001)..(825000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature

Query Match      2.4%; Score 32.8; DB 4; Length 1230025;
Best Local Similarity 59.8%; Pred. No. 99;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 224 TCGTCCCTTTTGAGGACCTCTCTGTTGTAGTGAAGACCTCGCGGATGATCTTCAG 283
DB 772064 TCCCTCCCTTTGACTCTGGAATCTATGCTATAGCAATGCTTAGCAATCACCTTCAG 772005

QY 284 CGCCACATCGAGGTATGAGAAAGCGGGA 315
DB 772004 CTGTTACTGCTGGTGGAGGAGATCGGCA 771973

RESULT 14
US-09-125-642C-9
; Sequence 9, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
; Their Production and Their Use in Vaccines
;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 100 Bayer Road
; CITY: Pittsburgh
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 15205-9741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,642C
; FILING DATE: 20-Aug-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00729,
; FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Parapox ovis
; STRAIN: D1701-Proteinkinase-Gen (Version 1)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-125-642C-2
Query Match      2.4%; Score 32.4; DB 4; Length 1620;
Best Local Similarity 46.8%; Pred. No. 4.3;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (810001)..(825000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature

Query Match      2.4%; Score 32.4; DB 4; Length 1620;
Best Local Similarity 46.8%; Pred. No. 4.3;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 870 CCGTGTCTGTTGATGCTCGACCGCAATGGGTGTCTCGAAACAATACCCAGGCTTCTTCA 929
DB 12 CCATCCCGTTGCTGGCGACTCGGACTGCCCTCTGTTTTTCTTCCGTTTCTTCTAT 71
QY 930 AAACATGACCTTACCACAATCGACCATCGGGGAAATCGCCAAACGAGTCACTGGGCGCAAC 989
DB 72 TAGGTAGTTGTTGCCACCTCCATGATCCTCGCAGCGCTGGCGGGCGACCTCGCACGCC 131
QY 990 AGCATCAGCGCTTCTGTTCCAGACTCGACCCCGCGAGCATGCGCCAGCAAGAGGTCT 1049
DB 132 CGCGCGCGCGCGCGCGCGCGCGCGAGGACGGAAGAACAGTGTATCGCCGGAAGCGCAAGCG 191
QY 1050 CGCGACGTACTGTCACAAACACCCCGCACAGTCCCAACG 1087
DB 192 CAAGACGCCCACTCGGAGACGCGGCACTCCGACG 229

RESULT 15
US-09-125-642C-2
; Sequence 2, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
; Their Production and Their Use in Vaccines
;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 100 Bayer Road
; CITY: Pittsburgh
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 15205-9741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,642C
; FILING DATE: 20-Aug-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00729,
; FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Parapox ovis
; STRAIN: D1701-Proteinkinase-Gen (Version 1)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-125-642C-2
Query Match      2.4%; Score 32.4; DB 4; Length 1740;
Best Local Similarity 46.8%; Pred. No. 4.5;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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QY 870 CCGTGTGTTGATGCTCGACCGCAATGGGTGTCTCGAACAACTACCCAGGCCCTTTCTCA 929
Db 12 CCATCCCGTTGCTGGGGACTCGGACTGCCCTCTGTTTTTCTTCCCGTTTCTCTTAT 71
QY 930 AAACATGACCTACCAAACTCGACCATCGGCGAAATCGCCAAAGTCACTCGGCGCAAC 989
Db 72 TAGGTAGTTGTTGCCACCTCCCATGATCTCGCACGCGCTGGCGGGCGAAGCTCGCACGCC 131
QY 990 AGCATCACGCTTGGTTTCAGAACTCGAACCCCGGAGCATGGCCAGCGAACAGAGTCT 1049
Db 132 CGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 191
QY 1050 CGCGACGTACTCTGCACAAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
Db 192 CAAGACGCCCAACTGCGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229

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Search completed: February 7, 2004, 23:22:31
 Job time : 104 secs